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(54) **POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND  
EXPRESSION OF SAME IN TRANSDUCED CELLS**

POLYNUKLEOTID KODIEREND FÜR EIN POLYPEPTID MIT HEPARANASE-AKTIVITÄT UND  
DESSEN EXPRESSION IN TRANSDUZIERTEN ZELLEN

POLYNUCLEOTIDE CODANT POUR UN POLYPEPTIDE PRESENTANT UNE ACTIVITE  
D'HEPARANASE ET SON EXPRESSION PAR DES CELLULES TRANSDUCTEES

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## Description

## FIELD AND BACKGROUND OF THE INVENTION

[0001] The present invention relates to a polynucleotide, referred to hereinbelow as *hpa*, encoding a polypeptide having heparanase activity, vectors including same and transduced cells expressing heparanase. The invention further relates to a recombinant protein having heparanase activity.

[0002] **Heparan sulfate proteoglycans:** Heparan sulfate proteoglycans (HSPG) are ubiquitous macromolecules associated with the cell surface and extra cellular matrix (ECM) of a wide range of cells of vertebrate and invertebrate tissues (1-4). The basic HSPG structure includes a protein core to which several linear heparan sulfate chains are covalently attached. These polysaccharide chains are typically composed of repeating hexuronic and D-glucosamine disaccharide units that are substituted to a varying extent with N- and O-linked sulfate moieties and N-linked acetyl groups (1-4). Studies on the involvement of ECM molecules in cell attachment, growth and differentiation revealed a central role of HSPG in embryonic morphogenesis, angiogenesis, neurite outgrowth and tissue repair (1-5). HSPG are prominent components of blood vessels (3). In large blood vessels they are concentrated mostly in the intima and inner media, whereas in capillaries they are found mainly in the subendothelial basement membrane where they support proliferating and migrating endothelial cells and stabilize the structure of the capillary wall. The ability of HSPG to interact with ECM macromolecules such as collagen, laminin and fibronectin, and with different attachment sites on plasma membranes suggests a key role for this proteoglycan in the self-assembly and insolubility of ECM components, as well as in cell adhesion and locomotion. Cleavage of the heparan sulfate (HS) chains may therefore result in degradation of the subendothelial ECM and hence may play a decisive role in extravasation of blood-borne cells. HS catabolism is observed in inflammation, wound repair, diabetes, and cancer metastasis, suggesting that enzymes which degrade HS play important roles in pathologic processes. Heparanase activity has been described in activated immune system cells and highly metastatic cancer cells (6-8), but research has been handicapped by the lack of biologic tools to explore potential causative roles of heparanase in disease conditions.

[0003] **Involvement of Heparanase in Tumor Cell Invasion and Metastasis:** Circulating tumor cells arrested in the capillary beds of different organs must invade the endothelial cell lining and degrade its underlying basement membrane (BM) in order to invade into the extravascular tissue(s) where they establish metastasis (9, 10). Metastatic tumor cells often attach at or near the intercellular junctions between adjacent endothelial cells. Such attachment of the metastatic cells is followed by rupture of the junctions, retraction of the endothelial cell borders and migration through the breach in the endothelium toward the exposed underlying BM (9). Once located between endothelial cells and the BM, the invading cells must degrade the subendothelial glycoproteins and proteoglycans of the BM in order to migrate out of the vascular compartment. Several cellular enzymes (e.g., collagenase IV, plasminogen activator, cathepsin B, elastase, etc.) are thought to be involved in degradation of BM (10). Among these enzymes is an endo- $\beta$ -D-glucuronidase (heparanase) that cleaves HS at specific intrachain sites (6, 8, 11). Expression of a HS degrading heparanase was found to correlate with the metastatic potential of mouse lymphoma (11), fibrosarcoma and melanoma (8) cells. Moreover, elevated levels of heparanase were detected in sera from metastatic tumor bearing animals and melanoma patients (8) and in tumor biopsies of cancer patients (12).

[0004] The control of cell proliferation and tumor progression by the local microenvironment, focusing on the interaction of cells with the extracellular matrix (ECM) produced by cultured corneal and vascular endothelial cells, was investigated previously by the present inventors. This cultured ECM closely resembles the subendothelium *in vivo* in its morphological appearance and molecular composition. It contains collagens (mostly type III and IV, with smaller amounts of types I and V), proteoglycans (mostly heparan sulfate- and dermatan sulfate- proteoglycans, with smaller amounts of chondroitin sulfate proteoglycans), laminin, fibronectin, entactin and elastin (13, 14). The ability of cells to degrade HS in the cultured ECM was studied by allowing cells to interact with a metabolically sulfate labeled ECM, followed by gel filtration (Sephacrose 6B) analysis of degradation products released into the culture medium (11). While intact HSPG are eluted next to the void volume of the column ( $K_{av} < 0.2$ ,  $M_r \sim 0.5 \times 10^6$ ), labeled degradation fragments of HS side chains are eluted more toward the  $V_t$  of the column ( $0.5 < k_{av} < 0.8$ ,  $M_r = 5 \times 10^3$ ) (11).

[0005] The heparanase inhibitory effect of various non-anticoagulant species of heparin that might be of potential use in preventing extravasation of blood-borne cells was also investigated by the present inventors. Inhibition of heparanase was best achieved by heparin species containing 16 sugar units or more and having sulfate groups at both the N and O positions. While O-desulfation abolished the heparanase inhibiting effect of heparin, O-sulfated, N-acetylated heparin retained a high inhibitory activity, provided that the N-substituted molecules had a molecular size of about 4,000 daltons or more (7). Treatment of experimental animals with heparanase inhibitors (e.g., non-anticoagulant species of heparin) markedly reduced (>90%) the incidence of lung metastases induced by B16 melanoma, Lewis lung carcinoma and mammary adenocarcinoma cells (7, 8, 16). Heparin fractions with high and low affinity to anti-thrombin III exhibited a comparable high anti-metastatic activity, indicating that the heparanase inhibiting activity of heparin, rather than its anticoagulant activity, plays a role in the anti-metastatic properties of the polysaccharide (7).

**[0006] Heparanase activity in the urine of cancer patients:** In an attempt to further elucidate the involvement of heparanase in tumor progression and its relevance to human cancer, urine samples for heparanase activity were screened (16a). Heparanase activity was detected in the urine of some, but not all, cancer patients. High levels of heparanase activity were determined in the urine of patients with an aggressive metastatic disease and there was no detectable activity in the urine of healthy donors.

**[0007]** Heparanase activity was also found in the urine of 20% of normal and microalbuminuric insulin dependent diabetes mellitus (IDDM) patients, most likely due to diabetic nephropathy, the most important single disorder leading to renal failure in adults.

**[0008] Possible involvement of heparanase in tumor angiogenesis:** Fibroblast growth factors are a family of structurally related polypeptides characterized by high affinity to heparin (17). They are highly mitogenic for vascular endothelial cells and are among the most potent inducers of neovascularization (17, 18). Basic fibroblast growth factor (bFGF) has been extracted from the subendothelial ECM produced *in vitro* (19) and from basement membranes of the cornea (20), suggesting that ECM may serve as a reservoir for bFGF. Immunohistochemical staining revealed the localization of bFGF in basement membranes of diverse tissues and blood vessels (21). Despite the ubiquitous presence of bFGF in normal tissues, endothelial cell proliferation in these tissues is usually very low, suggesting that bFGF is somehow sequestered from its site of action. Studies on the interaction of bFGF with ECM revealed that bFGF binds to HSPG in the ECM and can be released in an active form by HS degrading enzymes (15, 20, 22). It was demonstrated that heparanase activity expressed by platelets, mast cells, neutrophils, and lymphoma cells is involved in release of active bFGF from ECM and basement membranes (23), suggesting that heparanase activity may not only function in cell migration and invasion, but may also elicit an indirect neovascular response. These results suggest that the ECM HSPG provides a natural storage depot for bFGF and possibly other heparin-binding growth promoting factors (24, 25). Displacement of bFGF from its storage within basement membranes and ECM may therefore provide a novel mechanism for induction of neovascularization in normal and pathological situations.

**[0009]** Recent studies indicate that heparin and HS are involved in binding of bFGF to high affinity cell surface receptors and in bFGF cell signaling (26, 27). Moreover, the size of HS required for optimal effect was similar to that of HS fragments released by heparanase (28). Similar results were obtained with vascular endothelial cells growth factor (VEGF) (29), suggesting the operation of a dual receptor mechanism involving HS in cell interaction with heparin-binding growth factors. It is therefore proposed that restriction of endothelial cell growth factors in ECM prevents their systemic action on the vascular endothelium, thus maintaining a very low rate of endothelial cells turnover and vessel growth. On the other hand, release of bFGF from storage in ECM as a complex with HS fragment, may elicit localized endothelial cell proliferation and neovascularization in processes such as wound healing, inflammation and tumor development (24, 25).

**[0010] Expression of heparanase by cells of the immune system:** Heparanase activity correlates with the ability of activated cells of the immune system to leave the circulation and elicit both inflammatory and autoimmune responses. Interaction of platelets, granulocytes, T and B lymphocytes, macrophages and mast cells with the subendothelial ECM is associated with degradation of HS by a specific heparanase activity (6). The enzyme is released from intracellular compartments (e.g., lysosomes, specific granules, etc.) in response to various activation signals (e.g., thrombin, calcium ionophore, immune complexes, antigens, mitogens, etc.), suggesting its regulated involvement in inflammation and cellular immunity.

**Some of the observations regarding the heparanase enzyme were reviewed in reference No. 6 and are listed hereinbelow:**

**[0011]** First, a proteolytic activity (plasminogen activator) and heparanase participate synergistically in sequential degradation of the ECM HSPG by inflammatory leukocytes and malignant cells.

**[0012]** Second, a large proportion of the platelet heparanase exists in a latent form, probably as a complex with chondroitin sulfate. The latent enzyme is activated by tumor cell-derived factor(s) and may then facilitate cell invasion through the vascular endothelium in the process of tumor metastasis.

**[0013]** Third, release of the platelet heparanase from  $\alpha$ -granules is induced by a strong stimulant (i.e., thrombin), but not in response to platelet activation on ECM.

**[0014]** Fourth, the neutrophil heparanase is preferentially and readily released in response to a threshold activation and upon incubation of the cells on ECM.

**[0015]** Fifth, contact of neutrophils with ECM inhibited release of noxious enzymes (proteases, lysozyme) and oxygen radicals, but not of enzymes (heparanase, gelatinase) which may enable diapedesis. This protective role of the subendothelial ECM was observed when the cells were stimulated with soluble factors but not with phagocytosable stimulants.

**[0016]** Sixth, intracellular heparanase is secreted within minutes after exposure of T cell lines to specific antigens.

**[0017]** Seventh, mitogens (Con A, LPS) induce synthesis and secretion of heparanase by normal T and B lymphocytes maintained *in vitro*. T lymphocyte heparanase is also induced by immunization with antigen *in vivo*.

**[0018]** Eighth, heparanase activity is expressed by pre-B lymphomas and B-lymphomas, but not by plasmacytomas

and resting normal B lymphocytes.

[0019] Ninth, heparanase activity is expressed by activated macrophages during incubation with ECM, but there was little or no release of the enzyme into the incubation medium. Similar results were obtained with human myeloid leukemia cells induced to differentiate to mature macrophages.

[0020] Tenth, T-cell mediated delayed type hypersensitivity and experimental autoimmunity are suppressed by low doses of heparanase inhibiting non-anticoagulant species of heparin (30).

[0021] Eleventh, heparanase activity expressed by platelets, neutrophils and metastatic tumor cells releases active bFGF from ECM and basement membranes. Release of bFGF from storage in ECM may elicit a localized neovascular response in processes such as wound healing, inflammation and tumor development.

[0022] Twelfth, among the breakdown products of the ECM generated by heparanase is a tri-sulfated disaccharide that can inhibit T-cell mediated inflammation *in vivo* (31). This inhibition was associated with an inhibitory effect of the disaccharide on the production of biologically active TNF $\alpha$  by activated T cells *in vitro* (31).

[0023] **Other potential therapeutic applications:** Apart from its involvement in tumor cell metastasis, inflammation and autoimmunity, mammalian heparanase may be applied to modulate: bioavailability of heparin-binding growth factors (15); cellular responses to heparin-binding growth factors (e.g., bFGF, VEGF) and cytokines (IL-8) (31 a, 29); cell interaction with plasma lipoproteins (32); cellular susceptibility to certain viral and some bacterial and protozoa infections (33, 33a, 33b); and disintegration of amyloid plaques (34). Heparanase may thus prove useful for conditions such as wound healing, angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases and viral infections. Mammalian heparanase can be used to neutralize plasma heparin; as a potential replacement of protamine. Anti-heparanase antibodies may be applied for immunodetection and diagnosis of micrometastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples, and body fluids. Common use in basic research is expected.

[0024] The identification of the *hpa* gene encoding for heparanase enzyme will enable the production of a recombinant enzyme in heterologous expression systems. Availability of the recombinant protein will pave the way for solving the protein structure function relationship and will provide a tool for developing new inhibitors.

[0025] **Viral Infection:** The presence of heparan sulfate on cell surfaces have been shown to be the principal requirement for the binding of Herpes Simplex (33) and Dengue (33a) viruses to cells and for subsequent infection of the cells. Removal of the cell surface heparan sulfate by heparanase may therefore abolish virus infection. In fact, treatment of cells with bacterial heparitinase (degrading heparan sulfate) or heparinase (degrading heparan) reduced the binding of two related animal herpes viruses to cells and rendered the cells at least partially resistant to virus infection (33). There are some indications that the cell surface heparan sulfate is also involved in HIV infection (33b).

[0026] **Neurodegenerative diseases:** Heparan sulfate proteoglycans were identified in the prion protein amyloid plaques of Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease and Scrape (34). Heparanase may disintegrate these amyloid plaques which are also thought to play a role in the pathogenesis of Alzheimer's disease.

[0027] **Restenosis and Atherosclerosis:** Proliferation of arterial smooth muscle cells (SMCs) in response to endothelial injury and accumulation of cholesterol rich lipoproteins are basic events in the pathogenesis of atherosclerosis and restenosis (35). Apart from its involvement in SMC proliferation (i.e., low affinity receptors for heparin-binding growth factors), HS is also involved in lipoprotein binding, retention and uptake (36). It was demonstrated that HSPG and lipoprotein lipase participate in a novel catabolic pathway that may allow substantial cellular and interstitial accumulation of cholesterol rich lipoproteins (32). The latter pathway is expected to be highly atherogenic by promoting accumulation of apoB and apoE rich lipoproteins (i.e. LDL, VLDL, chylomicrons), independent of feed back inhibition by the cellular sterol content. Removal of SMC HS by heparanase is therefore expected to inhibit both SMC proliferation and lipid accumulation and thus may halt the progression of restenosis and atherosclerosis.

[0028] There is thus a widely recognized need for, and it would be highly advantageous to have a polynucleotide encoding a polypeptide having heparanase activity, vectors including same, transduced cells expressing heparanase and a recombinant protein having heparanase activity.

#### SUMMARY OF THE INVENTION

[0029] According to the present invention there is provided a polynucleotide, referred to hereinbelow as *hpa*, *hpa* cDNA or *hpa* gene, encoding a polypeptide having heparanase activity, vectors including same, transduced cells expressing heparanase and a recombinant protein having heparanase activity.

[0030] Cloning of the human *hpa* gene which encodes heparanase, and expression of recombinant heparanase by transfected host cells is reported.

[0031] A purified preparation of heparanase isolated from human hepatoma cells was subjected to tryptic digestion and microsequencing. The YGPDVGQPR (SEQ ID NO:8) sequence revealed was used to screen EST databases for homology to the corresponding back translated DNA sequence. Two closely related EST sequences were identified and were thereafter found to be identical. Both clones contained an insert of 1020 bp which included an open reading frame of 973 bp followed by a 27 bp of 3' untranslated region and a Poly. A tail. Translation start site was not identified.

**[0032]** Cloning of the missing 5' end of *hpa* was performed by PCR amplification of DNA from placenta Marathon RACE (RIM) cDNA composite using primers selected according to the EST clones sequence and the linkers of the composite. A 900 bp PCR fragment, partially overlapping with the identified 3' encoding EST clones was obtained. The joined cDNA fragment (*hpa*), 1721 bp long (SEQ ID NO:9), contained an open reading frame which encodes a polypeptide of 543 amino acids (SEQ ID NO:10) with a calculated molecular weight of 61,192 daltons.

**[0033]** Cloning an extended 5' sequence was enabled from the human SK-hepl cell line by PCR amplification using the Marathon RACE (RIM). The 5' extended sequence of the SK-hep 1 *hpa* cDNA was assembled with the sequence of the *hpa* cDNA isolated from human placenta (SEQ ID NO:9). The assembled sequence contained an open reading frame, SEQ ID NOs: 13 and 15, which encodes, as shown in SEQ ID NOs: 14 and 15, a polypeptide of 592 amino acids with, a calculated molecular weight of 66,407 daltons.

**[0034]** The ability of the *hpa* gene product to catalyze degradation of heparan sulfate in an *in vitro* assay was examined by expressing the entire open reading frame of *hpa* in insect cells, using the Baculovirus expression system. Extracts and conditioned media of cells infected with virus containing the *hpa* gene, demonstrated a high level of heparan sulfate degradation activity both towards soluble ECM-derived HSPG and intact ECM. This degradation activity was inhibited by heparin, which is another substrate of heparanase. Cells infected with a similar construct containing no *hpa* gene had no such activity, nor did non-infected cells. The ability of heparanase expressed from the extended 5' clone towards heparin was demonstrated in a mammalian expression system.

**[0035]** The expression pattern of *hpa* RNA in various tissues and cell lines was investigated using RT-PCR. It was found to be expressed only in tissues and cells previously known to have heparanase activity.

**[0036]** A panel of monochromosomal human/CHO and human/mouse somatic cell hybrids was used to localize the human heparanase gene to human chromosome 4. The newly isolated heparanase sequence can be used to identify a chromosome region harboring a human heparanase gene in a chromosome spread.

**[0037]** According to further features in preferred embodiments of the invention described below, there is provided a polynucleotide fragment which includes a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity.

**[0038]** According to still further features in the described preferred embodiments the polynucleotide fragment includes nucleotides 63-1691 of SEQ ID NO:9 or nucleotides 139-1869 of SEQ ID NO:13, which encode the entire human heparanase enzyme.

**[0039]** According to still further features in the described preferred embodiments there is provided a polynucleotide fragment which includes a polynucleotide sequence capable of hybridizing with *hpa* cDNA, especially with nucleotides 1-721 of SEQ ID NO:9.

**[0040]** According to still further features in the described preferred embodiments the polynucleotide sequence which encodes the polypeptide having heparanase activity shares at least 60 % homology, preferably at least 70 % homology, more preferably at least 80 % homology, most preferably at least 90 % homology with SEQ ID NOs:9 or 13.

**[0041]** According to still further features in the described preferred embodiments the polynucleotide fragment according to the present invention includes a portion (fragment) of SEQ ID NOs:9, or 13. For example, such fragments could include nucleotides 63-721 of SEQ ID NO:9 and/or a segment of SEQ ID NO:9 which encodes a polypeptide having the heparanase catalytic activity.

**[0042]** According to still further features in the described preferred embodiments the polypeptide encoded by the polynucleotide fragment includes an amino acid sequence as set forth in SEQ ID NOs:10 or 14 or a functional part thereof.

**[0043]** According to still further features in the described preferred embodiments the polynucleotide sequence encodes a polypeptide having heparanase activity, which shares at least 60 % homology, preferably at least 70 % homology, more preferably at least 80 % homology, most preferably at least 90 % homology with SEQ ID NOs:10 or 14.

**[0044]** According to still further features in the described preferred embodiments the polynucleotide fragment encodes a polypeptide having heparanase activity, which may therefore be allelic, species and/or induced variant of the amino acid sequence set forth in SEQ ID NOs:10 or 14. It is understood that any such variant may also be considered a homolog.

**[0045]** According to still further features in the described preferred embodiments there is provided a single stranded polynucleotide fragment which includes a polynucleotide sequence complementary to at least a portion of a polynucleotide strand encoding a polypeptide having heparanase catalytic activity as described above.

**[0046]** According to still further features in the described preferred embodiments there is provided a vector including a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity.

**[0047]** The vector may be of any suitable type including but not limited to a phage, virus, plasmid, phagemid, cosmid, bacmid or even an artificial chromosome. The polynucleotide sequence encoding a polypeptide having heparanase catalytic activity may include any of the above described polynucleotide fragments.

**[0048]** According to still further features in the described preferred embodiments there is provided a host cell which includes an exogenous polynucleotide fragment including a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity.

**[0049]** The exogenous polynucleotide fragment may be any of the above described fragments. The host cell may be

of any type such as prokaryotic cell, eukaryotic cell, a cell line, or a cell as a portion of a multicellular organism (e.g., cells of a transgenic organism).

[0050] According to still further features in the described preferred embodiments there is provided a recombinant protein including a polypeptide having heparanase catalytic activity.

[0051] According to still further features in the described preferred embodiments there is provided a pharmaceutical composition comprising as an active ingredient a recombinant protein having heparanase catalytic activity.

[0052] According to still further features in the described preferred embodiments there is provided a medical equipment comprising a medical device containing, as an active ingredient a recombinant protein having heparanase catalytic activity.

[0053] According to still further features in the described preferred embodiments there is provided a heparanase overexpression system comprising a cell overexpressing heparanase catalytic activity.

[0054] According to still further features in the described preferred embodiments there is provided a method of identifying a chromosome region harboring a human heparanase gene in a chromosome spread comprising the steps of (a) hybridizing the chromosome spread with a tagged polynucleotide probe encoding heparanase; (b) washing the chromosome spread, thereby removing excess of non-hybridized probe; and (c) searching for signals associated with said hybridized tagged polynucleotide probe, wherein detected signals being indicative of a chromosome region harboring a human heparanase gene.

[0055] The present invention can be used to develop new drugs to inhibit tumor cell metastasis, inflammation and autoimmunity. The identification of the *hpa* gene encoding for heparanase enzyme enables the production of a recombinant enzyme in heterologous expression systems.

#### BRIEF DESCRIPTION OF THE DRAWINGS

[0056] The invention herein described, by way of example only, with reference to the accompanying drawings, wherein:

FIG. 1 presents nucleotide sequence and deduced amino acid sequence of *hpa* cDNA. A single nucleotide difference at position 799 (A to T) between the EST (Expressed Sequence Tag) and the PCR amplified cDNA (reverse transcribed RNA) and the resulting amino acid substitution (Tyr to Phe) are indicated above and below the substituted unit, respectively. Cysteine residues and the poly adenylation consensus sequence are underlined. The asterisk denotes the stop codon TGA.

FIG. 2 demonstrates degradation of soluble sulfate labeled HSPG substrate by lysates of High Five (RIM) cells infected with pFhpa2 virus. Lysates of High Five (RIM) cells that were infected with pFhpa2 virus (•) or control pF2 virus (□) were incubated (18 h, 37 °C) with sulfate labeled ECM-derived soluble HSPG (peak I). The incubation medium was then subjected to gel filtration on Sepharose 6B. Low molecular weight HS degradation fragments (peak II) were produced only during incubation with the pFhpa2 infected cells, but there was no degradation of the HSPG substrate (♦) by lysates of pF2 infected cells.

FIGs. 3a-b demonstrate degradation of soluble sulfate labeled HSPG substrate by the culture medium of pFhpa2 and pFhpa4 infected cells. Culture media of High Five (RIM) cells infected with pFhpa2 (3a) or pFhpa4 (3b) viruses (•), or with control viruses (□) were incubated (18 h, 37 °C) with sulfate labeled ECM-derived soluble HSPG (peak I, ♦). The incubation media were then subjected to gel filtration on Sepharose 6B. Low molecular weight HS degradation fragments (peak II) were produced only during incubation with the *hpa* gene containing viruses. There was no degradation of the HSPG substrate by the culture medium of cells infected with control viruses.

FIG. 4 presents size fractionation of heparanase activity expressed by pFhpa2 infected cells. Culture medium of pFhpa2 infected High Five (RIM) cells was applied onto a 50 kDa cut-off membrane. Heparanase activity (conversion of the peak I substrate, (♦) into peak II HS degradation fragments) was found in the high (> 50 kDa) (•), but not low (< 50 kDa) (o) molecular weight compartment.

FIGs. 5a-b demonstrate the effect of heparin on heparanase activity expressed by pFhpa2 and pFhpa4 infected High Five (RIM) cells. Culture media of pFhpa2 (5a) and pFhpa4 (5b) infected High Five (RIM) cells were incubated (18 h, 37 °C) with sulfate labeled ECM-derived soluble HSPG (peak I, ♦) in the absence (•) or presence (Δ) of 10 μg/ml heparin. Production of low molecular weight HS degradation fragments was completely abolished in the presence of heparin, a potent inhibitor of heparanase activity (6, 7).

FIGs. 6a-b demonstrate degradation of sulfate labeled intact ECM by virus infected High Five (RIM) and Sf21 Cells. High Five (RIM) (6a) and Sf21 (6b) cells were plated on sulfate labeled ECM and infected (48 h, 28 °C) with pFhpa4 (•) or control pF1 (□) viruses. Control non-infected Sf21 cells (R) were plated on the labeled ECM as well. The pH of the cultured medium was adjusted to 6.0 - 6.2 followed by 24 h incubation at 37 °C. Sulfate labeled material released into the incubation medium was analyzed by gel filtration on Sepharose 6B. HS degradation fragments were produced only by cells infected with the *hpa* containing virus.

FIG. 7a-b demonstrate degradation of sulfate labeled intact ECM by virus infected cells. High Five (RIM) (7a) and

Sf21 (7b) cells were plated on sulfate labeled ECM and infected (48 h, 28 °C) with pFhpa4 (•) or control pF1 (□) viruses. Control non-infected Sf21 cells (R) were plated on labeled ECM as well. The pH of the cultured medium was adjusted to 6.0 - 6.2, followed by 48 h incubation at 28 °C. Sulfate labeled degradation fragments released into the incubation medium were analyzed by gel filtration on Sepharose 6B. HS degradation fragments were produced only by cells infected with the *hpa* containing virus.

FIGs. 8a-b demonstrate degradation of sulfate labeled intact ECM by the culture medium of pFhpa4 infected cells. Culture media of High Five (RIM) (8a) and Sf21 (8b) cells that were infected with pFhpa4 (•) or control pF1 (□) viruses were incubated (48 h, 37 °C, pH 6.0) with intact sulfate labeled ECM. The ECM was also incubated with the culture medium of control non-infected Sf21 cells (R). Sulfate labeled material released into the reaction mixture was subjected to gel filtration analysis. Heparanase activity was detected only in the culture medium of pFhpa4 infected cells.

FIGs. 9a-b demonstrate the effect of heparin on heparanase activity in the culture medium of pFhpa4 infected cells. Sulfate labeled ECM was incubated (24 h, 37 °C, pH 6.0) with culture medium of pFhpa4 infected High Five (RIM) (9a) and Sf21 (9b) cells in the absence (•) or presence (V) of 10 µg/ml heparin. Sulfate labeled material released into the incubation medium was subjected to gel filtration on Sepharose 6B. Heparanase activity (production of peak II HS degradation fragments) was completely inhibited in the presence of heparin.

FIGs. 10a-b demonstrate purification of recombinant heparanase on heparin-Sepharose. Culture medium of Sf21 cells infected with pFhpa4 virus was subjected to heparin-Sepharose chromatography. Elution of fractions was performed with 0.3 - 2 M NaCl gradient (♦). Heparanase activity in the eluted fractions is demonstrated in Figure 10a (•). Fractions 15-28 were subjected to 15% SDS-polyacrylamide gel electrophoresis followed by silver nitrate staining. A correlation is demonstrated between a major protein band (MW ~ 63,000) in fractions 19-24 and heparanase activity.

FIGs. 11a-b demonstrate purification of recombinant heparanase on a Superdex 75 gel filtration column. Active fractions eluted from heparin-Sepharose (Figure 10a) were pooled, concentrated and applied onto Superdex 75 FPLC column. Fractions were collected and aliquots of each fraction were tested for heparanase activity (C, Figure 11a) and analyzed by SDS-polyacrylamide gel electrophoresis followed by silver nitrate staining (Figure 11b). A correlation is seen between the appearance of a major protein band (MW ~ 63,000) in fractions 4 - 7 and heparanase activity.

FIGs. 12a-e demonstrate expression of the *hpa* gene by RT-PCR with total RNA from human embryonal tissues (12a), human extra-embryonal tissues (12b) and cell lines from different origins (12c-e). RT-PCR products using *hpa* specific primers (I), primers for GAPDH housekeeping gene (II), and control reactions without reverse transcriptase demonstrating absence of genomic DNA or other contamination in RNA samples (III). M- DNA molecular weight marker VI (Boehringer Mannheim). For 12a: lane 1 - neutrophil cells (adult), lane 2 - muscle, lane 3 - thymus, lane 4 - heart, lane 5 - adrenal. For 12b: lane 1 - kidney, lane 2 - placenta (8 weeks), lane 3 - placenta (11 weeks), lanes 4-7 - mole (complete hydatidiform mole), lane 8 - cytotrophoblast cells (freshly isolated), lane 9 - cytotrophoblast cells (1.5 h *in vitro*), lane 10 - cytotrophoblast cells (6 h *in vitro*), lane 11 - cytotrophoblast cells (18 h *in vitro*), lane 12 - cytotrophoblast cells (48 h *in vitro*). For 12c: lane 1 - JAR bladder cell line, lane 2 - NCITT testicular tumor cell line, lane 3 - SW-480 human hepatoma cell line, lane 4 - HTR (cytotrophoblasts transformed by SV40), lane 5 - HPTLP-1 hepatocellular carcinoma cell line, lane 6 - EJ-28 bladder carcinoma cell line. For 12d: lane 1 - SK-hep-1 human hepatoma cell line, lane 2 - DAMI human megakaryocytic cell line, lane 3 - DAMI cell line + PMA, lane 4 - CHRF cell line + PMA, lane 5 - CHRF cell line. For 12e: lane 1 - ABAE bovine aortic endothelial cells, lane 2 - 1063 human ovarian cell line, lane 3 - human breast carcinoma MDA435 cell line, lane 4 - human breast carcinoma MDA231 cell line.

FIG. 13 presents a comparison between nucleotide sequences of the human *hpa* and a mouse EST cDNA fragment (SEQ ID NO:12) which is 80 % homologous to the 3' end (starting at nucleotide 1066 of SEQ ID NO:9) of the human *hpa*. The aligned termination codons are underlined.

FIG. 14 demonstrates the chromosomal localization of the *hpa* gene. PCR products of DNA derived from somatic cell hybrids and of genomic DNA of hamster, mouse and human were separated on 0.7 % agarose gel following amplification with *hpa* specific primers. Lane 1 - Lambda DNA digested with *Bst*EII, lane 2 - no DNA control, lanes 3 - 29, PCR amplification products. Lanes 3-5 - human, mouse and hamster genomic DNA, respectively. Lanes 6-29, human monochromosomal somatic cell hybrids representing chromosomes 1-22 and X and Y, respectively. Lane 30 - Lambda DNA digested with *Bst*EII. An amplification product of approximately 2.8 Kb is observed only in lanes 5 and 9, representing human genomic DNA and DNA derived from cell hybrid carrying human chromosome 4, respectively. These results demonstrate that the *hpa* gene is localized in human chromosome 4.

#### DESCRIPTION OF THE PREFERRED EMBODIMENTS

[0057] The present invention is of a polynucleotide, referred to hereinbelow interchangeably as *hpa*, *hpa* cDNA or



*hpa* gene, encoding a polypeptide having heparanase activity, vectors including same, transduced cells expressing heparanase and a recombinant protein having heparanase activity.

**[0058]** Before explaining at least one embodiment of the invention in detail, it is to be understood that the invention is not limited in its application to the details of construction and the arrangement of the components set forth in the following description or illustrated in the drawings.

**[0059]** Also, it is to be understood that the phraseology and terminology employed herein is for the purpose of description and should not be regarded as limiting.

**[0060]** The present invention can be used to develop treatments for various diseases, to develop diagnostic assays for these diseases and to provide new tools for basic research especially in the fields of medicine and biology.

**[0061]** Specifically, the present invention can be used to develop new drugs to inhibit tumor cell metastasis, inflammation and autoimmunity. The identification of the *hpa* gene encoding for the heparanase enzyme enables the production of a recombinant enzyme in heterologous expression systems.

**[0062]** Furthermore, the present invention can be used to modulate bioavailability of heparin-binding growth factors, cellular responses to heparin-binding growth factors (e.g., bFGF, VEGF) and cytokines (IL-8), cell interaction with plasma lipoproteins, cellular susceptibility to viral, protozoa and some bacterial infections, and disintegration of neurodegenerative plaques. Recombinant heparanase is thus a potential treatment for wound healing, angiogenesis, restenosis, atherosclerosis, inflammation, neurodegenerative diseases (such as, for example, Genstmann-Straussler Syndrome, Creutzfeldt-Jakob disease, Scrapie and Alzheimer's disease) and certain viral and some bacterial and protozoa infections. Recombinant heparanase can be used to neutralize plasma heparin, as a potential replacement of protamine.

**[0063]** As used herein, the term "modulate" includes substantially inhibiting, slowing or reversing the progression of a disease, substantially ameliorating clinical symptoms of a disease or condition, or substantially preventing the appearance of clinical symptoms of a disease or condition. A "modulator" therefore includes an agent which may modulate a disease or condition. Modulation of viral, protozoa and bacterial infections includes any effect which substantially interrupts, prevents or reduces any viral, bacterial or protozoa activity and/or stage of the virus, bacterium or protozoon life cycle, or which reduces or prevents infection by the virus, bacterium or protozoon in a subject, such as a human or lower animal.

**[0064]** As used herein, the term "wound" includes any injury to any portion of the body of a subject including, but not limited to, acute conditions such as thermal burns, chemical burns, radiation burns, burns caused by excess exposure to ultraviolet radiation such as sunburn, damage to bodily tissues such as the perineum as a result of labor and childbirth, including injuries sustained during medical procedures such as episiotomies, trauma-induced injuries including cuts, those injuries sustained in automobile and other mechanical accidents, and those caused by bullets, knives and other weapons, and post-surgical injuries, as well as chronic conditions such as pressure sores, bedsores, conditions related to diabetes and poor circulation, and all types of acne, etc.

**[0065]** Anti-heparanase antibodies, raised against the recombinant enzyme, would be useful for immunodetection and diagnosis of micrometastases, autoimmune lesions and renal failure in biopsy specimens, plasma samples, and body fluids. Such antibodies may also serve as neutralizing agents for heparanase activity.

**[0066]** Cloning of the human *hpa* gene encoding heparanase and expressing recombinant heparanase by transfected cells is herein reported. This is the first mammalian heparanase gene to be cloned.

**[0067]** A purified preparation of heparanase isolated from human hepatoma cells was subjected to tryptic digestion and microsequencing.

**[0068]** The YGPDVGQPR (SEQ ID NO:8) sequence revealed was used to screen EST databases for homology to the corresponding back translated DNA sequences. Two closely related EST sequences were identified and were thereafter found to be identical.

**[0069]** Both clones contained an insert of 1020 bp which includes an open reading frame of 973 bp followed by a 3' untranslated region of 27 bp and a Poly A tail, whereas a translation start site was not identified.

**[0070]** Cloning of the missing 5' end was performed by PCR amplification of DNA from placenta marathon RACE (RIM) cDNA composite using primers selected according to the EST clones sequence and the linkers of the composite.

**[0071]** A 900 bp PCR fragment, partially overlapping with the identified 3' encoding EST clones was obtained. The joined cDNA fragment (*hpa*), 1721 bp long (SEQ ID NO:9), contained an open reading frame which encodes, as shown in Figure 1 and SEQ ID NO:11, a polypeptide of 543 amino acids (SEQ ID NO:10) with a calculated molecular weight of 61,192 daltons.

**[0072]** A single nucleotide difference at position 799 (A to T) between the EST clones and the PCR amplified cDNA was observed. This difference results in a single amino acid substitution (Tyr to Phe) (Figure 1). Furthermore, the published EST sequences contained an unidentified nucleotide, which following DNA sequencing of both the EST clones was resolved into two nucleotides (G and C at positions 1630 and 1631 in SEQ ID NO:9, respectively).

**[0073]** The ability of the *hpa* gene product to catalyze degradation of heparan sulfate in an *in vitro* assay was examined by expressing the entire open reading frame in insect cells, using the Baculovirus expression system.

**[0074]** Extracts and conditioned media of cells infected with virus containing the *hpa* gene, demonstrated a high level

of heparan sulfate degradation activity both towards soluble ECM-derived HSPG and intact ECM, which was inhibited by heparin, while cells infected with a similar construct containing no *hpa* gene had no such activity, nor did non-infected cells.

**[0075]** The expression pattern of *hpa* RNA in various tissues and cell lines was investigated using RT-PCR. It was found to be expressed only in tissues and cells previously known to have heparanase activity.

**[0076]** Cloning an extended 5' sequence was enabled from the human SK-hep1 cell line by PCR amplification using the Marathon RACE (RIM) The 5' extended sequence of the SK-hep1 *hpa* cDNA was assembled with the sequence of the *hpa* cDNA isolated from human placenta (SEQ ID NO:9). The assembled sequence contained an open reading frame, SEQ ID NOs: 13 and 15, which encodes, as shown in SEQ ID NOs:14 and 15, a polypeptide of 592 amino acids, with a calculated molecular weight of 66,407 daltons. This open reading frame was shown to direct the expression of catalitically active heparanase in a mammalian cell expression system. The expressed heparanase was detectable by anti heparanase antibodies in Western blot analysis.

**[0077]** A panel of monochromosomal human/CHO and human/mouse somatic cell hybrids was used to localize the human heparanase gene to human chromosome 4. The newly isolated heparanase sequence can therefore be used to identify a chromosome region harboring a human heparanase gene in a chromosome spread.

**[0078]** Thus, according to the present invention there is provided a polynucleotide fragment (either DNA or RNA, either single stranded or double stranded) which includes a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity.

**[0079]** The term "heparanase catalytic activity" or its equivalent term "heparanase activity" both refer to a mammalian endoglycosidase hydrolyzing activity which is specific for heparan or heparan sulfate proteoglycan substrates, as opposed to the activity of bacterial enzymes (heparinase I, II and III) which degrade heparin or heparan sulfate by means of  $\beta$ -elimination (37).

**[0080]** In a preferred embodiment of the invention the polynucleotide fragment includes nucleotides 63-1691 of SEQ ID NO:9, or nucleotides 139-1869 of SEQ ID NO: 13, which encode the entire human heparanase enzyme.

**[0081]** However, the scope of the present invention is not limited to human heparanase since this is the first disclosure of an open reading frame (ORF) encoding any mammalian heparanase. Using the *hpa* cDNA, parts thereof or synthetic oligonucleotides designed according to its sequence will enable one ordinarily skilled in the art to identify genomic and/or cDNA clones including homologous sequences from other mammalian species.

**[0082]** The present invention is therefore further directed at a polynucleotide fragment which includes a polynucleotide sequence capable of hybridizing (base pairing under either stringent or permissive hybridization conditions, as for example described in Sambrook, J.; Fritsch, E.F., Maniatis, T. (1989) Molecular Cloning. A Laboratory Manual. Cold Spring Harbor Laboratory Press, New York.) with *hpa* cDNA, especially with nucleotides 1-721 of SEQ ID NO:9.

**[0083]** In fact, any polynucleotide sequence which encodes a polypeptide having heparanase activity and which shares at least 60 % homology, preferably at least 70 % homology, more preferably at least 80 % homology, most preferably at least 90 % homology with SEQ ID NOs:9 or 13 is within the scope of the present invention.

**[0084]** The polynucleotide fragment according to the present invention may include any part of SEQ ID NOs: 9 or 13. For example, it may include nucleotides 63-721 of SEQ ID NO:9, which is a novel sequence. However, it may include any segment of SEQ ID NOs:9 or 13 which encodes a polypeptide having the heparanase catalytic activity.

**[0085]** When the phrase "encodes a polypeptide having heparanase catalytic activity" is used herein and in the claims section below it refers to the ability of directing the synthesis of a polypeptide which, if so required for its activity, following post translational modifications, such as but not limited to, proteolysis (e.g., removal of a signal peptide and of a pro- or preprotein sequence), methionine modification, glycosylation, alkylation (e.g., methylation), acetylation, etc., is catalytically active in degradation of, for example, ECM and cell surface associated HS.

**[0086]** In a preferred embodiment of the invention the polypeptide encoded by the polynucleotide fragment includes an amino acid sequence as set forth in SEQ ID NOs:10 or 14 or a functional part thereof, i.e., a portion harboring heparanase catalytic activity.

**[0087]** However, any polynucleotide fragment which encodes a polypeptide having heparanase activity is within the scope of the present invention. Therefore, the polypeptide may be allelic, species and/or induced variant of the amino acid sequence set forth in SEQ ID NOs: 10 or 14 or functional part thereof.

**[0088]** In fact, any polynucleotide sequence which encodes a polypeptide having heparanase activity, which shares at least 60 % homology, preferably at least 70 % homology, more preferably at least 80 % homology, most preferably at least 90 % homology with SEQ ID NOs:10 or 14 is within the scope of the present invention.

**[0089]** The invention is also directed at providing a single stranded polynucleotide fragment which includes a polynucleotide sequence complementary to at least a portion of a polynucleotide strand encoding a polypeptide having heparanase catalytic activity as described above. The term "complementary" as used herein refers to the ability of base pairing.

**[0090]** The single stranded polynucleotide fragment may be DNA or RNA or even include nucleotide analogs (e.g., thioated nucleotides), it may be a synthetic oligonucleotide or manufactured by transduced host cells, it may be of any desired length which still provides specific base pairing (e.g., 8 or 10, preferably more, nucleotides long) and it may

include mismatches that do not hamper base pairing.

**[0091]** The invention is further directed at providing a vector which includes a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity.

**[0092]** The vector may be of any type. It may be a phage which infects bacteria or a virus which infects eukaryotic cells. It may also be a plasmid, phagemid, cosmid, bacmid or an artificial chromosome. The polynucleotide sequence encoding a polypeptide having heparanase catalytic activity may include any of the above described polynucleotide fragments.

**[0093]** The invention is further directed at providing a host cell which includes an exogenous polynucleotide fragment encoding a polypeptide having heparanase catalytic activity.

**[0094]** The exogenous polynucleotide fragment may be any of the above described fragments. The host cell may be of any type. It may be a prokaryotic cell, an eukaryotic cell, a cell line, or a cell as a portion of an organism. The exogenous polynucleotide fragment may be permanently or transiently present in the cell. In other words, transduced cells obtained following stable or transient transfection, transformation or transduction are all within the scope of the present invention. The term "exogenous" as used herein refers to the fact that the polynucleotide fragment is externally introduced into the cell. Therein it may be present in a single of any number of copies, it may be integrated into one or more chromosomes at any location or be present as an extrachromosomal material.

**[0095]** The invention is further directed at providing a heparanase overexpression system which includes a cell overexpressing heparanase catalytic activity. The cell may be a host cell transiently or stably transfected or transformed with any suitable vector which includes a polynucleotide sequence encoding a polypeptide having heparanase activity and a suitable promoter and enhancer sequences to direct overexpression of heparanase. However, the overexpressing cell may also be a product of an insertion (e.g., via homologous recombination) of a promoter and/or enhancer sequence upstream to the endogenous heparanase gene of the expressing cell, which will direct overexpression from the endogenous gene. The term "overexpression" as used herein in the specification and claims below refers to a level of expression which is higher than a basal level of expression typically characterizing a given cell under otherwise identical conditions.

**[0096]** The invention is further directed at providing a recombinant protein including a polypeptide having heparanase catalytic activity.

**[0097]** The recombinant protein may be purified by any conventional protein purification procedure close to homogeneity and/or be mixed with additives. The recombinant protein may be manufactured using any of the cells described above. The recombinant protein may be in any form. It may be in a crystallized form, a dehydrated powder form or in solution. The recombinant protein may be useful in obtaining pure heparanase, which in turn may be useful in eliciting anti-heparanase antibodies, either poly or monoclonal antibodies, and as a screening active ingredient in an anti-heparanase inhibitors or drugs screening assay or system.

**[0098]** The invention is further directed at providing a pharmaceutical composition which include as an active ingredient a recombinant protein having heparanase catalytic activity.

**[0099]** Formulations for topical administration may include, but are not limited to, lotions, ointments, gels, creams, suppositories, drops, liquids, sprays and powders. Conventional pharmaceutical carriers, aqueous, powder or oily bases, thickeners and the like may be necessary or desirable. Coated condoms, stents, active pads, and other medical devices may also be useful. In fact the scope of the present invention includes any medical equipment such as a medical device containing, as an active ingredient, a recombinant protein having heparanase catalytic activity.

**[0100]** Compositions for oral administration include powders or granules, suspensions or solutions in water or non-aqueous media, sachets, capsules or tablets. Thickeners, diluents, flavorings, dispersing aids, emulsifiers or binders may be desirable.

**[0101]** Formulations for parenteral administration may include, but are not limited to; sterile aqueous solutions which may also contain buffers, diluents and other suitable additives.

**[0102]** Dosing is dependent on severity and responsiveness of the condition to be treated, but will normally be one or more doses per day, with course of treatment lasting from several days to several months or until a cure is effected or a diminution of disease state is achieved. Persons ordinarily skilled in the art can easily determine optimum dosages, dosing methodologies and repetition rates.

**[0103]** Further according to the present invention there is provided a method of identifying a chromosome region harboring a human heparanase gene in a chromosome spread. the method is executed implementing the following method steps, in which in a first step the chromosome spread (either interphase or metaphase spread) is hybridized with a tagged polynucleotide probe encoding heparanase. The tag is preferably a fluorescent tag. In a second step according to the method the chromosome spread is washed, thereby excess of non-hybridized probe is removed. Finally, signals associated with the hybridized tagged polynucleotide probe are searched for, wherein detected signals being indicative of a chromosome region harboring the human heparanase gene. One ordinarily skilled in the art would know how to use the sequences disclosed herein in suitable labeling reactions and how to use the tagged probes to detect, using *in situ* hybridization, a chromosome region harboring a human heparanase gene.

**[0104]** Reference is now made to the following examples, which together with the above descriptions, illustrate the

invention in a non-limiting fashion.

## EXAMPLES

[0105] The following protocols and experimental details are referenced in the Examples that follow:

[0106] **Purification and characterization of heparanase from a human hepatoma cell line and human placenta:**

A human hepatoma cell line (Sk-hep-1) was chosen as a source for purification of a human tumor-derived heparanase. Purification was essentially as described in U.S. Pat. No. 5,362,641 to Fuks.

[0107] Briefly, 500 liter,  $5 \times 10^{11}$  cells were grown in suspension and the heparanase enzyme was purified about 240,000 fold by applying the following steps: (i) cation exchange (CM-Sephadex) chromatography performed at pH 6.0, 0.3-1.4 M NaCl gradient; (ii) cation exchange (CM-Sephadex) chromatography performed at pH 7.4 in the presence of 0.1% CHAPS, 0.3-1.1 M NaCl gradient; (iii) heparin-Sepharose chromatography performed at pH 7.4 in the presence of 0.1% CHAPS, 0.35-1.1 M NaCl gradient; (iv) ConA-Sepharose chromatography performed at pH 6.0 in buffer containing 0.1% CHAPS and 1 M NaCl, elution with 0.25 M  $\alpha$ -methyl mannoside; and (v) HPLC cation exchange (Mono-S) chromatography performed at pH 7.4 in the presence of 0.1% CHAPS, 0.25-1 M NaCl gradient.

[0108] Active fractions were pooled, precipitated with TCA and the precipitate subjected to SDS polyacrylamide gel electrophoresis and/or tryptic digestion and reverse phase HPLC. Tryptic peptides of the purified protein were separated by reverse phase HPLC (C8 column) and homogeneous peaks were subjected to amino acid sequence analysis.

[0109] The purified enzyme was applied to reverse phase HPLC and subjected to N-terminal amino acid sequencing using the amino acid sequencer (Applied Biosystems).

[0110] **Cells:** Cultures of bovine corneal endothelial cells (BCECs) were established from steer eyes as previously described (19, 38). Stock cultures were maintained in DMEM (1 g glucose/liter) supplemented with 10% newborn calf serum and 5% FCS. bFGF (1 ng/ml) was added every other day during the phase of active cell growth (13,14).

[0111] **Preparation of dishes coated with ECM:** BCECs (second to fifth passage) were plated into 4-well plates at an initial density of  $2 \times 10^5$  cells/ml, and cultured in sulfate-free Fisher medium plus 5% dextran T-40 for 12 days.  $\text{Na}_2^{35}\text{SO}_4$  (25  $\mu\text{Ci/ml}$ ) was added on day 1 and 5 after seeding and the cultures were incubated with the label without medium change. The subendothelial ECM was exposed by dissolving (5 min., room temperature) the cell layer with PBS containing 0.5% Triton. X-100 and 20 mM  $\text{NH}_4\text{OH}$ , followed by four washes with PBS. The ECM remained intact; free of cellular debris and firmly attached to the entire area of the tissue culture dish (19, 22).

[0112] To prepare soluble sulfate labeled proteoglycans (peak I material), the ECM was digested with trypsin (25  $\mu\text{g/ml}$ , 6 h, 37 °C), the digest was concentrated by reverse dialysis and the concentrated material was applied onto a Sepharose 6B gel filtration column. The resulting high molecular weight material ( $K_{av} < 0.2$ , peak I) was collected. More than 80% of the labeled material was shown to be composed of heparan sulfate proteoglycans (11, 39).

[0113] **Heparanase activity:** Cells ( $1 \times 10^6/35\text{-mm}$  dish), cell lysates or conditioned media were incubated on top of  $^{35}\text{S}$ -labeled ECM (18 h, 37 °C) in the presence of 20 mM phosphate buffer (pH 6.2). Cell lysates and conditioned media were also incubated with sulfate labeled peak I material (10-20  $\mu\text{l}$ ). The incubation medium was collected, centrifuged (18,000  $\times g$ , 4 °C, 3 min.), and sulfate labeled material analyzed by gel filtration on a Sepharose CL-6B column (0.9  $\times$  30 cm). Fractions (0.2 ml) were eluted with PBS at a flow rate of 5 ml/h and counted for radioactivity using Bio-fluor scintillation fluid. The excluded volume ( $V_o$ ) was marked by blue dextran and the total included volume ( $V_t$ ) by phenol red. The latter was shown to comigrate with free sulfate (7, 11, 23). Degradation fragments of HS side chains were eluted from Sepharose 6B at  $0.5 < K_{av} < 0.8$  (peak II) (7, 11, 23). A nearly intact HSPG released from ECM by trypsin - and, to a lower extent, during incubation with PBS alone - was eluted next to  $V_o$  ( $K_{av} < 0.2$ , peak I). Recoveries of labeled material applied on the columns ranged from 85 to 95% in different experiments (11). Each experiment was performed at least three times and the variation of elution positions ( $K_{av}$  values) did not exceed  $\pm 15\%$ .

[0114] **Cloning of hpa cDNA:** cDNA clones 257548 and 260138 were obtained from the I.M.A.G.E Consortium (2130 Memorial Parkway SW, Huntsville, AL 35801). The cDNAs were originally cloned in *EcoRI* and *NotI* cloning sites in the plasmid vector pT3T7D-Pac. Although these clones are reported to be somewhat different, DNA sequencing demonstrated that these clones are identical to one another. Marathon RACE (RIM) (rapid amplification of cDNA ends) human placenta (poly-A) cDNA composite was a gift of Prof Yossi Shiloah of Tel Aviv University.. This composite is vector free, as it includes reverse transcribed cDNA fragments to which double, partially single stranded adapters are attached on both sides. The construction of the specific composite employed is described in reference 39a.

[0115] Amplification of hp3 PCR fragment was performed according to the protocol provided by Clontech laboratories. The template used for amplification was a sample taken from the above composite. The primers used for amplification were:

First step: 5'-primer: AP1: 5'-CCATCCTAATACGACTCACTATAGGG  
C-3', SEQ ID NO:1; 3'-primer: HPL229: 5'-GTAGTGATGCCATGTAAGTGA  
ATC-3', SEQ ID NO:2.

[0116] Second step: nested 5'-primer AP2: 5'-ACTCACTATAGGGCTCGAGCG GC-3', SEQ ID NO:3; nested 3'- primer: HPL171: 5'-GCATCTTAGCCGTCT TTCTTCG-3', SEQ ID NO:4. The HPL229 and HPL 171 were selected according to the sequence of the EST clones. They include nucleotides 933-956 and 876-897 of SEQ ID NO:9, respectively.

[0117] PCR program was 94 °C - 4 min., followed by 30 cycles of 94 °C - 40 sec., 62 °C - 1 min., 72°C - 2.5 min. Amplification was performed with Expand High Fidelity (Boehringer Mannheim). The resulting ca. 900 bp hp3 PCR product was digested with *Bfi*I and *Pvu*II. Clone 257548 (*phpa1*) was digested with *Eco*RI, followed by end filling and was then further digested with *Bfi*I. Thereafter the *Pvu*II - *Bfi*I fragment of the hp3 PCR product was cloned into the blunt end - *Bfi*I end of clone *phpa1* which resulted in having the entire cDNA cloned in pT3T7-pac vector, designated *phpa2*.

[0118] **DNA Sequencing:** Sequence determinations were performed with vector specific and gene specific primers, using an automated DNA sequencer (Applied Biosystems, model 373A). Each nucleotide was read from at least two independent primers.

[0119] **Computer analysis of sequences:** Database searches for sequence similarities were performed using the Blast network service. Sequence analysis and alignment of DNA and protein sequences were done using the DNA sequence analysis software package developed by the Genetic Computer Group (GCG) at the University of Wisconsin,

[0120] **RT-PCR:** RNA was prepared using TRI-Reagent (Molecular research center Inc.) according to the manufacturer instructions. 1.25 µg were taken for reverse transcription reaction using MuMLV Reverse transcriptase (Gibco BRL) and Oligo (dT)<sub>15</sub> primer, SEQ ID NO:5, (Promega). Amplification of the resultant first strand cDNA was performed with Taq polymerase (Promega). The following primers were used:

HPU-355: 5'-TTCGATCCCAAGAAGGAATCAAC-3', SEQ ID NO:6, nucleotides 372-394 in SEQ ID NO:9 or 11.

HPL-229: 5'-GTAGTGATGCCATGTAAGTGAATC-3', SEQ ID NO:7, nucleotides 933-956 in SEQ ID NO:9 or 11.

PCR program: 94 °C - 4 min., followed by 30 cycles of 94°C - 40 sec., 62°C - 1 min., 72°C - 1 min.

[0121] **Expression of recombinant heparanase in insect cells:** Cells, High Five (RIM) and Sf21 insect cell lines were maintained as monolayer cultures in SF900II-SFM medium (GibcoBRL).

[0122] **Recombinant Baculovirus:** Recombinant virus containing the *hpa* gene was constructed using the Bac to Bac system (GibcoBRL). The transfer vector pFastBac was digested with *Sa*I and *Not*I and ligated with a 1-7 kb fragment of *phpa2* digested with *Xho*I and *Not*I. The resulting plasmid was designated pFast*hpa2*. An identical plasmid designated pFast*hpa4* was prepared as a duplicate and both independently served for further experimentations. Recombinant bacmid was generated according to the instructions of the manufacturer with pFast*hpa2*, pFast*hpa4* and with pFastBac. The latter served as a negative control. Recombinant bacmid DNAs were transfected into Sf21 insect cells. Five days after transfection recombinant viruses were harvested and used to infect High Five (RIM) cells. 3 x 10<sup>6</sup> cells in T-25 flasks. Cells were harvested 2 - 3 days after infection. 4 x 10<sup>6</sup> cells were centrifuged and resuspended in a reaction buffer containing 20 mM phosphate citrate buffer, 50 mM NaCl. Cells underwent three cycles of freeze and thaw and lysates were stored at -80 °C. Conditioned medium was stored at 4 °C.

[0123] **Partial purification of recombinant heparanase:** Partial purification of recombinant heparanase was performed by heparin-Sepharose column chromatography followed by Superdex 75 column gel filtration. Culture medium (150 ml) of Sf21 cells infected with pFhpa4 virus was subjected to heparin-Sepharose chromatography. Elution of 1 ml fractions was performed with 0.35 - 2 M NaCl gradient in presence of 0.1 % CHAPS and 1 mM DTT in 10 mM sodium acetate buffer, pH 5.0. A 25 µl sample of each fraction was tested for heparanase activity. Heparanase activity was eluted at the range of 0.65 - 1.1 M NaCl (fractions 18-26, Figure 10a). 5 µl of each fraction was subjected to 15 % SDS-polyacrylamide gel electrophoresis followed by silver nitrate staining. Active fractions eluted from heparin-Sepharose (Figure 10a) were pooled and concentrated (x 6) on YM3 cut-off membrane. 0.5 ml of the concentrated material was applied onto 30 ml Superdex 75 FPLC column equilibrated with 10 mM sodium acetate buffer, pH 5.0, containing 0.8 M NaCl, 1 mM DTT and 0.1 % CHAPS. Fractions (0.56 ml) were collected at a flow rate of 0.75 ml/min. Aliquots of each fraction were tested for heparanase activity and were subjected to SDS-polyacrylamide gel electrophoresis followed by silver nitrate staining (Figure 11b).

**EXAMPLE 1****Cloning of the *hpa* gene**

**[0124]** Purified fraction of heparanase isolated from human hepatoma cells (SK-hep-1) was subjected to tryptic digestion and microsequencing. EST (Expressed Sequence Tag) databases were screened for homology to the back translated DNA sequences corresponding to the obtained peptides. Two EST sequences (accession Nos. N41349 and N45367) contained a DNA sequence encoding the peptide YGPDVGQPR (SEQ ID NO:8). These two sequences were derived from clones 257548 and 260138 (I.M.A.G.E Consortium) prepared from 8 to 9 weeks placenta cDNA library (Soares). Both clones which were found to be identical contained an insert of 1020 bp which included an open reading frame (ORF) of 973 bp followed by a 3' untranslated region of 27 bp and a Poly A tail. No translation start site (AUG) was identified at the 5' end of these clones.

**[0125]** Cloning of the missing 5' end was performed by PCR amplification of DNA from a placenta Marathon RACE (RIM) cDNA composite. A 900 bp fragment (designated hp3), partially overlapping with the identified 3' encoding EST clones was obtained

**[0126]** The joined cDNA fragment, 1721 bp long (SEQ ID NO:9), contained an open reading frame which encodes, as shown in Figure 1 and SEQ ID NO: 11, a polypeptide of 543 amino acids (SEQ ID NO:10) with a calculated molecular weight of 61,192 daltons. The 3' end of the partial cDNA inserts contained in clones 257548 and 260138 started, at nucleotide G<sup>721</sup> of SEQ ID NO:9 and Figure 1.

**[0127]** As further shown in Figure 1, there was a single sequence discrepancy between the EST clones and the PCR amplified sequence, which led to an amino acid substitution from Tyr<sup>246</sup> in the EST to Phe<sup>246</sup> in the amplified cDNA. The nucleotide sequence of the PCR amplified cDNA fragment was verified from two independent amplification products. The new gene was designated *hpa*.

**[0128]** As stated above, the 3' end of the partial cDNA inserts contained in EST clones 257548 and 260138 started at nucleotide 721 of *hpa* (SEQ ID NO:9). The ability of the *hpa* cDNA to form stable secondary structures, such as stem and loop structures involving nucleotide stretches in the vicinity of position 721 was investigated using computer modeling. It was found that stable stem and loop structures are likely to be formed involving nucleotides 698-724 (SEQ ID NO:9). In addition, a high GC content, up to 70 %, characterizes the 5' end region of the *hpa* gene, as compared to about only 40 % in the 3' region. These findings may explain the immature termination and therefore lack of 5' ends in the EST clones.

**[0129]** To examine the ability of the *hpa* gene product to catalyze degradation of heparan sulfate in an *in vitro* assay the entire open reading frame was expressed in insect cells, using the Baculovirus expression system. Extracts of cells, infected with virus containing the *hpa* gene, demonstrated a high level of heparan sulfate degradation activity, while cells infected with a similar construct containing no *hpa* gene had no such activity, nor did non-infected cells. These results are further demonstrated in the following Examples.

**EXAMPLE 2****Degradation of soluble ECM-derived HSPG**

**[0130]** Monolayer cultures of High Five (RIM) cells were infected (72 h, 28 °C) with recombinant Baculovirus containing the pFast*hpa* plasmid or with control virus containing an insert free plasmid. The cells were harvested and lysed in heparanase reaction buffer by three cycles of freezing and thawing. The cell lysates were then incubated (18 h, 37 °C) with sulfate labeled, ECM-derived HSPG (peak 1), followed by gel filtration analysis (Sephacrose 6B) of the reaction mixture.

**[0131]** As shown in Figure 2, the substrate alone included almost entirely high molecular weight (Mr) material eluted next to V<sub>0</sub> (peak I, fractions 5-20, Kav < 0.35). A similar elution pattern was obtained when the HSPG substrate was incubated with lysates of cells that were infected with control virus. In contrast, incubation of the HSPG substrate with lysates of cells infected with the *hpa* containing virus resulted in a complete conversion of the high Mr substrate into low Mr labeled degradation fragments (peak II, fractions 22-35, 0.5 < Kav < 0.75).

**[0132]** Fragments eluted in peak II were shown to be degradation products of heparan sulfate, as they were (i) 5- to 6-fold smaller than intact heparan sulfate side chains (Kav approx. 0.33) released from ECM by treatment with either alkaline borohydride or papain; and (ii) resistant to further digestion with papain or chondroitinase ABC, and susceptible to deamination by nitrous acid (6, 11).

**[0133]** Similar results (not shown) were obtained with Sf21 cells. Again, heparanase activity was detected in cells infected with the *hpa* containing virus (pF*hpa*), but not with control virus (pF). This result was obtained with two independently generated recombinant viruses. Lysates of control not infected High Five (RIM) cells failed to degrade the HSPG substrate.

**[0134]** In subsequent experiments, the labeled HSPG substrate was incubated with medium conditioned by infected

High Five (RIM) or Sf21 cells.

[0135] As shown in Figures 3a-b, heparanase activity, reflected by the conversion of the high Mr peak I substrate into the low Mr peak II which represents HS degradation fragments, was found in the culture medium of cells infected with the pFhpa2 or pFhpa4 viruses, but not with the control pF1 or pF2 viruses. No heparanase activity was detected in the culture medium of control non-infected High Five (RIM) or Sf21 cells.

[0136] The medium of cells infected with the pFhpa4 virus was passed through a 50 kDa cut off membrane to obtain a crude estimation of the molecular weight of the recombinant heparanase enzyme. As demonstrated in Figure 4, all the enzymatic activity was retained in the upper compartment and there was no activity in the flow through (<50 kDa) material. This result is consistent with the expected molecular weight of the hpa gene product.

[0137] In order to further characterize the hpa product the inhibitory effect of heparin, a potent inhibitor of heparanase mediated HS degradation (40) was examined.

[0138] As demonstrated in Figures 5a-b, conversion of the peak I substrate into peak II HS degradation fragments was completely abolished in the presence of heparin.

[0139] Altogether, these results indicate that the heparanase enzyme is expressed in an active form by insect cells infected with Baculovirus containing the newly identified human hpa gene.

### EXAMPLE 3

#### Degradation of HSPG in intact ECM

[0140] Next, the ability of intact infected insect cells to degrade HS in intact, naturally produced ECM was investigated. For this purpose, High Five (RIM) or Sf21 cells were seeded on metabolically sulfate labeled ECM followed by infection (48 h, 28 °C) with either the pFhpa4 or control pF2 viruses. The pH of the medium was then adjusted to pH 6.2-6.4 and the cells further incubated with the labeled ECM for another 48 h at 28 °C or 24 h at 37 °C. Sulfate labeled material released into the incubation medium was analyzed by gel filtration on Sepharose 6B.

[0141] As shown in Figures- 6a-b and 7a-b, incubation of the ECM with cells infected with the control pF2 virus resulted in a constant release of labeled material that consisted almost entirely (>90%) of high Mr fragments (peak I) eluted with or next to  $V_0$ . It was previously shown that a proteolytic activity residing in the ECM itself and/or expressed by cells is responsible for release of the high Mr material (6). This nearly intact HSPG provides a soluble substrate for subsequent degradation by heparanase, as also indicated by the relatively large amount of peak I material accumulating when the heparanase enzyme is inhibited by heparin (6, 7, 12, Figure 9). On the other hand, incubation of the labeled ECM with cells infected with the pFhpa4 virus resulted in release of 60-70% of the ECM-associated radioactivity in the form of low Mr sulfate-labeled fragments (peak II,  $0.5 < K_{av} < 0.75$ ), regardless of whether the infected cells were incubated with the ECM at 28 °C or 37 °C. Control intact non-infected Sf21 or High Five (RIM) cells failed to degrade the ECM HS side chains.

[0142] In subsequent experiments, as demonstrated in Figs. 8a-b, High Five (RIM) and Sf21 cells were infected (96 h, 28 °C) with pFhpa4 or control pF1 viruses and the culture medium incubated with sulfate-labeled ECM. Low Mr HS degradation fragments were released from the ECM only upon incubation with medium conditioned by pFhpa4 infected cells. As shown in Figure 9, production of these fragments was abolished in the presence of heparin. No heparanase activity was detected in the culture medium of control, non-infected cells. These results indicate that the heparanase enzyme expressed by cells infected with the pFhpa4 virus is capable of degrading HS when complexed to other macromolecular constituents (i.e. fibronectin, laminin, collagen) of a naturally produced intact ECM, in a manner similar to that reported for highly metastatic tumor cells or activated cells of the immune system (6; 7).

### EXAMPLE 4

#### Purification of recombinant heparanase

[0143] The recombinant heparanase was partially purified from medium of pFhpa4 infected Sf21 cells by Heparin-Sepharose chromatography (Figure 10a) followed by gel filtration of the pooled active fractions over an FPLC Superdex 75 column (Figure 11a). A ~ 63 kDa protein was observed, whose quantity, as was detected by silver stained SDS-polyacrylamide gel electrophoresis, correlated with heparanase activity in the relevant column fractions (Figures 10b and 11b, respectively). This protein was not detected in the culture medium of cells infected with the control pF1 virus and was subjected to a similar fractionation on heparin-Sepharose (not shown).

**EXAMPLE 5****Expression of the *hpa* gene in various cell types, organs and tissues**

[0144] Referring now to Figures 12a-e, RT-PCR was applied to evaluate the expression of the *hpa* gene by various cell types and tissues. For this purpose, total RNA was reverse transcribed and amplified. The expected 585 bp long cDNA was clearly demonstrated in human kidney, placenta (8 and 11 weeks) and mole tissues, as well as in freshly isolated and short termed (1.5-48 h) cultured human placental cytotrophoblastic cells (Figure 12a), all known to express a high heparanase activity (41). The *hpa* transcript was also expressed by normal human neutrophils (Figure 12b). In contrast, there was no detectable expression of the *hpa* mRNA in embryonic human muscle tissue, thymus, heart and adrenal. (Figure 12b). The *hpa* gene was expressed by several, but not all, human bladder carcinoma cell lines (Figure 12c), SK hepatoma (SK-hep-1), ovarian carcinoma (OV 1063), breast carcinoma (435, 231), melanoma and megakaryocytic (DAMI, CHRF) human cell lines (Figures 12d-e).

[0145] The above described expression pattern of the *hpa* transcript was determined to be in a very good correlation with heparanase activity levels determined in various tissues and cell types (not shown).

**EXAMPLE 6*****hpa* homologous genes**

[0146] EST databases were screened for sequences homologous to the *hpa* gene. Three mouse ESTs were identified (accession No. Aa177901, from mouse spleen, Aa067997 from mouse skin, Aa47943 from mouse embryo), assembled into a 824 bp cDNA fragment which contains a partial open reading frame (lacking a 5' end) of 629 bp and a 3' untranslated region of 195 bp (SEQ ID NO:12). As shown in Figure 13, the coding region is 80% similar to the 3' end of the *hpa* cDNA sequence. These ESTs are probably cDNA fragments of the mouse *hpa* homolog that encodes for the mouse heparanase.

[0147] Searching for consensus protein domains revealed an amino terminal homology between the heparanase and several precursor proteins such as Procollagen Alpha 1 precursor, Tyrosine-protein kinase-RYK, Fibulin-1, Insulin-like growth factor binding protein and several others. The amino terminus is highly hydrophobic and contains a potential trans-membrane domain. The homology to known signal peptide sequences suggests that it could function as a signal peptide for protein localization.

**EXAMPLE 7*****Isolation of an extended 5' end of hpa cDNA from human SK-hep1 cell line***

[0148] The 5' end of *hpa* cDNA was isolated from human SK-hep1 cell line by PCR amplification using the Marathon RACE (RIM) (rapid amplification of cDNA ends) kit (Clontech). Total RNA was prepared from SK-hep1 cells using the TRI-Reagent (Molecular research center Inc.) according to the manufacturer instructions. Poly A+ RNA was isolated using the mRNA separator kit (Clontech).

[0149] The Marathon RACE SK-hep1 cDNA composite was constructed according to the manufacturer recommendations. First round of amplification was performed using an adaptor specific primer AP1: 5'-CCATCCTAATACG ACT-CACTATAGGGC-3', SEQ ID NO:1, and a *hpa* specific antisense primer hpl-629: 5'-CCCCAGGAGCAGCAGCATCAG-3', SEQ ID NO:17, corresponding to nucleotides 119-99 of SEQ ID NO:9. The resulting PCR product was subjected to a second round of amplification using an adaptor specific nested primer AP2: 5'-ACTCACTATAGGGCTCGAGCGGC-3', SEQ ID NO:3, and a *hpa* specific antisense nested primer hpl-666 5'-AGGCTTCGAGCGCAGCAGCAT-3', SEQ ID NO:18, corresponding to nucleotides 83-63 of SEQ ID NO:9. The PCR program was as follows: a hot start of 94 °C for 1 minute, followed by 30 cycles of 90 °C - 30 seconds, 68 °C - 4 minutes. The resulting 300 bp DNA fragment was extracted from an agarose gel and cloned into the vector pGEM-T Easy (Promega). The resulting recombinant plasmid was designated pHPSK1.

[0150] The nucleotide sequence of the pHPSK1 insert was determined and it was found to contain 62 nucleotides of the 5' end of the placenta *hpa* cDNA (SEQ ID NO:9) and additional 178 nucleotides upstream, the first 178 nucleotides of SEQ ID NOs:13 and 15.

[0151] A single nucleotide discrepancy was identified between the SK-hep1 cDNA and the placenta cDNA. The "T" derivative at position 9 of the placenta cDNA (SEQ ID NO:9), is replaced by a "C" derivative at the corresponding position 187 of the SK-hep cDNA (SEQ ID NO: 13).

[0152] The discrepancy is likely to be due to a mutation at the 5' end of the placenta cDNA clone as confirmed by sequence analysis of several additional cDNA clones isolated from placenta, which like the SK-hep1 cDNA contained C at position 9 of SEQ ID NO:9..



[0153] The 5' extended sequence of the SK-hepl *hpa* cDNA was assembled with the sequence of the *hpa* cDNA isolated from human placenta (SEQ ID NO:9). The assembled sequence contained an open reading frame which encodes, as shown in SEQ ID NOs:14 and 15, a polypeptide of 592 amino acids with a calculated molecular weight of 66,407 daltons. The open reading frame is flanked by 93 bp 5' untranslated region (UTR).

## EXAMPLE 8

### *Isolation of the upstream genomic region of the hpa gene*

[0154] The upstream region of the *hpa* gene was isolated using the Genome Walker kit (Clontech) according to the manufacturer recommendations. The kit includes five human genomic DNA samples each digested with a different restriction endonuclease creating blunt ends: *EcoRV*, *Scal*, *DraI*, *PvuII* and *SspI*.

[0155] The blunt ended DNA fragments are ligated to partially single stranded adaptors. The Genomic DNA samples were subjected to PCR amplification using the adaptor specific primer and a gene specific primer. Amplification was performed with Expand High Fidelity (Boehringer Mannheim).

[0156] A first round of amplification was performed using the ap1 primer: 5'-G TAATACGACTCACTATAGGGC-3', SEQ ID NO:19, and the *hpa* specific antisense primer hpl-666: 5'-AGGCTTCGAGCGCAGCAGCAT-3', SEQ ID NO:18, corresponding to nucleotides 83—63 of SEQ ID NO:9. The PCR program was as follows: a hot start of 94 °C - 3 minutes, followed by 36 cycles of 94 °C - 40 seconds, 67 °C - 4 minutes.

[0157] The PCR products of the first amplification were diluted 1:50. One µl of the diluted sample was used as a template for a second amplification using a nested adaptor specific primer ap2: 5'-ACTATAGGGCAGCGTGGT-3', SEQ ID NO:20, and a *hpa* specific antisense primer hpl-690, 5'-CTTGGGCTCACC TGGCTGCTC-3', SEQ ID NO:21, corresponding to nucleotides 62-42 of SEQ ID NO:9. The resulting amplification products were analyzed using agarose gel electrophoresis. Five different PCR products were obtained from the five amplification reactions. A DNA fragment of approximately 750 bp which was obtained from the *SspI* digested DNA sample was gel extracted. The purified fragment was ligated into the plasmid vector pGEM-T Easy (Promega). The resulting recombinant plasmid was designated pGHP6905 and the nucleotide sequence of the *hpa* insert was determined.

[0158] A partial sequence of 594 nucleotides is shown in SEQ ID NO:16. The last nucleotide in SEQ ID NO:13 corresponds to nucleotide 93 in SEQ ID:13. The DNA sequence in SEQ ID NO:16 contains the 5' region of the *hpa* cDNA and 501 nucleotides of the genomic upstream region which are predicted to contain the promoter region of the *hpa* gene.

## EXAMPLE 9

### *Expression of the 592 amino acids HPA polypeptide in a human 293 cell line*

[0159] The 592 amino acids open reading frame (SEQ ID NOs:13 and 15) was constructed by ligation of the 110 bp corresponding to the 5' end of the SK-hep 1 *hpa* cDNA with the placenta cDNA. More specifically the Marathon RACE (RIM) PCR amplification product of the placenta *hpa* DNA was digested with *SacI* and an approximately 1 kb fragment was ligated into a *SacI*-digested pGHP6905 plasmid. The resulting plasmid was digested with *EatI* and *AatII*. The *EatI* sticky ends were blunted and an approximately 280 bp *EatI*/blunt-*AatII* fragment was isolated. This fragment was ligated with pFast*hpa* digested with *EcoRI* which was blunt ended using Klenow fragment and further digested with *AatII*. The resulting plasmid contained a 1827 bp insert which includes an open reading frame of 1776 bp, 31 bp of 3' UTR and 21 bp of 5' UTR. This plasmid was designated pFast*Lhpa*.

[0160] A mammalian expression vector was constructed to drive the expression of the 592 amino acids heparanase polypeptide in human cells. The *hpa* cDNA was excised from pFast*Lhpa* with *BssHII* and *NotI*. The resulting 1850 bp *BssHII*-*NotI* fragment was ligated to a mammalian expression vector pSI (Promega) digested with *MluI* and *NotI*. The resulting recombinant plasmid, pSI*hpaMet2* was transfected into a human 293 embryonic kidney cell line.

[0161] Transient expression of the 592 amino-acids heparanase was examined by western blot analysis and the enzymatic activity was tested using the gel shift assay. Both these procedures are described in length in U.S. Pat. application No. 09/071,739, filed May 1, 1998, which is incorporated by reference as if fully set forth herein. Cells were harvested 3 days following transfection. Harvested cells were re-suspended in lysis buffer containing 150 mM NaCl, 50 mM Tris pH 7.5, 1% Triton X-100, 1 mM PMSF and protease inhibitor cocktail (Boehringer Mannheim). 40 µg protein extract samples were used for separation on a SDS-PAGE. Proteins were transferred onto a PVDF Hybond-P membrane (Amersham). The membrane was incubated with an affinity purified polyclonal anti heparanase antibody, as described in U.S. Pat. application No. 09/071,739. A major band of approximately 50 kDa was observed in the transfected cells as well as a minor band of approximately 65 kDa. A similar pattern was observed in extracts of cells transfected with the p*Shpa* as demonstrated in U.S. Pat application No. 09/071,739. These two bands probably represent two forms of

the recombinant heparanase protein produced by the transfected cells. The 65 kDa protein probably represents a heparanase precursor, while the 50 kDa protein is suggested herein to be the processed or mature form.

[0162] The catalytic activity of the recombinant protein expressed in the pS*hpa*Met2 transfected cells was tested by gel shift assay. Cell extracts of transfected and of mock transfected cells were incubated overnight with heparin (6 µg in each reaction) at 37 °C, in the presence of 20 mM phosphate citrate buffer pH 5.4, 1 mM CaCl<sub>2</sub>, 1 mM DTT and 50 mM NaCl. Reaction mixtures were then separated on a 10 % polyacrylamide gel. The catalytic activity of the recombinant heparanase was clearly demonstrated by a faster migration of the heparin molecules incubated with the transfected cell extract as compared to the control. Faster migration indicates the disappearance of high molecular weight heparin molecules and the generation of low molecular weight degradation products.

## EXAMPLE 10

### *Chromosomal localization of the hpa gene*

[0163] Chromosomal mapping of the *hpa* gene was performed utilizing a panel of monochromosomal human/CHO and human/mouse somatic cell hybrids, obtained from the UK HGMP Resource Center (Cambridge, England).

[0164] 40 ng of each of the somatic cell hybrid DNA samples were subjected to PCR amplification using the *hpa* primers: hpu565 5'-AGCTCTGTAGATGTGC TATACAC-3', SEQ ID NO:22, corresponding to nucleotides 564-586 of SEQ ID NO:9 and an antisense primer hpl171 5'-GCATCTTAGCCGTCTTCTTCG-3', SEQ ID NO:23, corresponding to nucleotides 897-876 of SEQ ID NO:9.

[0165] The PCR program was as follows: a hot start of 94 °C - 3 minutes, - followed by 7 cycles of 94 °C - 45 seconds, 66 °C - 1 minute, 68 °C - 5 minutes, followed by 30 cycles of 94 °C - 45 seconds, 62°C - 1 minute, 68°C - 5 minutes, and a 10 minutes final extension at 72°C.

[0166] The reactions were performed with Expand long PCR (Boehringer Mannheim). The resulting amplification products were analyzed using agarose gel electrophoresis. As demonstrated in Figure 14, a single band of approximately 2.8 Kb was obtained from chromosome 4, as well as from the control human genomic DNA. A 2.8 kb amplification product is expected based on amplification of the genomic *hpa* clone (data not shown). No amplification products were obtained neither in the control DNA samples of hamster and mouse nor in somatic hybrids of other human chromosome.

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# SEQUENCE LISTING

[0168]

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Iris Pecker, Israel Vlodavsky and Elena Feinstein
- (ii) TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY AND EXPRESSION OF SAME IN TRANSDUCED CELLS
- (iii) NUMBER OF SEQUENCES: 23
- (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Mark M. Friedman c/o Robert Sheinbein
- (B) STREET: 2940 Birchtree lane
- (C) CITY: Silver Spring
- (D) STATE: Maryland
- (E) COUNTRY: United States of America
- (F) ZIP: 20906

## (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
- (B) COMPUTER: Twinhead\* Slimnote-890TX
- (C) OPERATING SYSTEM: MS DOS version 6.2, Windows version 3.11
- (D) SOFTWARE: Word for Windows version 2.0 converted to an ASCII file

## (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/922,170
- (B) FILING DATE: 2 SEP 1997

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Friedman, Mark M.
- (B) REGISTRATION NUMBER: 33,883
- (C) REFERENCE/DOCKET NUMBER: 910/1

## (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 972-3-5625553
- (B) TELEFAX: 972-3-5625554
- (C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D.) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

**CCATCCTAAT ACGACTCACT ATAGGGC 27**

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

**GTAGTGATGC CATGTAAC TG AATC 24**

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

**ACTCACTATA GGGCTCGAGC GGC 23**

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

**GCATCTTAGC CGTCTTTC TT CG 22**

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ 10 NO:5:

TTTTTTTTTT TTTT 15

(2) INFORMATION FOR SEQ 10 NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTCGATCCCA AGAAGGAATC AAC 23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTAGTGATGC CATGTAACG AATC 24

(2) INFORMATION FOR SEQ 10 NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Tyr Gly Pro Asp Val Gly Gln Pro Arg  
5 9

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1721
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

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AGATGCTGCT GCGCTCGAAG CCTGCGCTGC CGCGCCGCT GATGCTGCTG CTCCTGGGGC 120
CGCTGGGTCC CCTCTCCCTT GCGCGCCTGC CCCGACCTGC GCAAGCACAG GACGTCGTGG 180
ACCTGGACTT CTTCACCCAG GAGCCGCTGC ACCTGGTGAG CCCCTCGTTC CTGTCCGTCA 240
CCATTGACGC CAACCTGGCC ACGGACCCGC GGTTCTCAT CCTCCTGGGT TCTCCAAAGC 300
TTCTGTACCTT GGCCAGAGGC TTGTCTCCTG CGTACCTGAG GTTTGGTGGC ACCAAGACAG 360
ACTTCCTAAT TTTCGATCCC AAGAAGGAAT CAACCTTTGA AGAGAGAAAT TACTGGCAAT 420
CTCAAGTCAA CCAGGATATT TGCAAATATG GATCCATCCC TCCTGATGTG GAGGAGAAGT 480
TACGGTTGGA ATGGCCCTAC CAGGAGCAAT TGCTACTCCG AGAACACTAC CAGAAAAAGT 540
TCAAGAACAG CACCTACTCA AGAAGCTCTG TAGATGTGCT ATACACTTTT GCAAACTGCT 600
CAGGACTGGA CTGTATCTTT GGCCTAAATG CGTTATTAAG AACAGCAGAT TTGCAGTGGG 660
ACAGTTCTAA TGCTCAGTTG CTCCTGGACT ACTGCTCTTC CAAGGGGTAT AACATTTCTT 720
GGGAACATAGG CAATGAACCT AACAGTTTCC TTAAGAAGGC TGATATTTTC ATCAATGGGT 780
CGCAGTTAGG AGAAGATTAT ATTCAATTGC ATAAACTTCT AAGAAAGTCC ACCTTCAAAA 840
ATGCAAAACT CTATGGTCCT GATGTTGGTC AGCCTCGAAG AAAGACGGCT AAGATGCTGA 900
AGAGCTTCCT GAAGGCTGGT GGAGAAGTGA TTGATTTCAGT TACATGGCAT CACTACTATT 960
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TTTCATCTGT GCAAAAAGTT TTCCAGGTGG TTGAGAGCAC CAGGCCTGGC AAGAAAGTCT 1080
GGTTAGGAGA AACAAGCTCT GCATATGGAG GCGGAGCGCC CTTGCTATCC GACACCTTTG 1140
CAGCTGGCTT TATGTGGCTG GATAAATTGG GCCTGTCAGC CCGAATGGGA ATAGAAGTGG 1200
TGATGAGGCA AGTATTCTTT GGAGCAGGAA ACTACCATTT AGTGGATGAA AACTTCGATC 1260
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TGGCAAGCGT GCAAGGTICA AAGAGAAGGA AGCTTCGAGT ATACCTTCAI TGCACAAACA 1380
CTGACAATCC AAGGTATAAA GAAGGAGATT TAACTCTGTA TGCCATAAAC CTCCATAACG 1440
TCACCAAGTA CTTCGGGTTA CCTATCCTT TTTCTAACAA GCAAGTGGAT AAATACCTTC 1500
TAAGACCTTT GGGACCTCAT GGATTAATTT CCAAATCTGT CCAACTCAAT GGTCTAACTC 1560
TAAAGATGGT GGATGATCAA ACCTTGCCAC CTTTAATGGA AAAACCTCTC CGGCCAGGAA 1620
GTTCACTGGG CTTGCCAGCT TTCTCATATA GTTTTTTTGT GATAAGAAAT GCCAAAGTTG 1680
CTGCTTGCAI CTGAAAATAA AATATACTAG TCCTGACACT G 1721

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ 10 NO:10:



EP 0 998 569 B1

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5 10 15

Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro  
20 25 30

Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro  
35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe  
100 105 110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys  
115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp  
130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe  
145 150 155 160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe  
165 170 175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu  
180 185 190

Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu  
195 200 205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn  
210 215 220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser  
225 230 235 240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser  
245 250 255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg  
260 265 270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu  
275 280 285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr  
290 295 300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile  
305 310 315 320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly  
325 330 335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala  
340 345 350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys  
355 360 365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val

370                      375                      380  
 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro  
 385                      390                      395                      400  
 5      Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr  
                                  405                      410                      415  
 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg  
                                  420                      425                      430  
 10     Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly  
                                  435                      440                      445  
 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu  
                                  450                      455                      460  
 15     Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu  
                                  465                      470                      475                      480  
 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn  
                                  485                      490                      495  
 20     Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met  
                                  500                      505                      510  
 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser  
                                  515                      520                      525  
 25     Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile  
                                  530                      535                      540                      543

(2) INFORMATION FOR SEQ ID NO:11:

30      (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1718  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35      (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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**EP 0 998 569 B1**

CT AGA GCT TTC GAC 14

TCT CCG CTG CGC GGC AGC TGG CGG GGG GAG CAG CCA GGT GAG CCC AAG 62

ATG CTG CTG CCG TCG AAG CCT GCG CTG CCG CCG CCG CTG ATG CTG CTG 110  
Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu  
5 10 15

CTC CTG GGG CCG CTG GGT CCC CTC TCC CCT GGC GCC CTG CCC CGA CCT 158  
Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro  
20 25 30

GCG CAA GCA CAG GAC GTC GTG GAC CTG GAC TTC TTC ACC CAG GAG CCG 206  
Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro  
35 40 45

CTG CAC CTG GTG AGC CCC TCG TTC CTG TCC GTC ACC ATT GAC GCC AAC 254  
Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
50 55 60

CTG GCC ACG GAC CCG CGG TTC CTC ATC CTC CTG GGT TCT CCA AAG CTT 302  
Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
65 70 75 80

CGT ACC TTG GCC AGA GGC TTG TCT CCT GCG TAC CTG AGG TTT GGT GGC 350  
Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
85 90 95

ACC AAG ACA GAC TTC CTA ATT TTC GAT CCC AAG AAG GAA TCA ACC TTT 398  
Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe  
100 105 110

GAA GAG AGA AGT TAC TGG CAA TCT CAA GTC AAC CAG GAT ATT TGC AAA 446  
Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys  
115 120 125

EP 0 998 569 B1

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TAT GGA TCC ATC CCT CCT GAT GTG GAG GAG AAG TTA CGG TTG GAA TGG 494  
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130 135 140

CCC TAC CAG GAG CAA TTG CTA CTC CGA GAA CAC TAC CAG AAA AAG TTC 542  
Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe  
145 150 155 160

AAG AAC AGC ACC TAC TCA AGA AGC TCT GTA GAT GTG CTA TAC ACT TTT 590  
Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe  
165 170 175

GCA AAC TGC TCA GGA CTG GAC TTG ATC TTT GGC CTA AAT GCG TTA TTA 638  
Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu  
180 185 190

AGA ACA GCA GAT TTG CAG TGG AAC AGT TCT AAT GCT CAG TTG CTC CTG 686  
Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu  
195 200 205

GAC TAC TGC TCT TCC AAG GGG TAT AAC ATT TCT TGG GAA CTA GGC AAT 734  
Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn  
210 215 220

GAA CCT AAC AGT TTC CTT AAG AAG GCT GAT ATT TTC ATC AAT GGG TCG 782  
Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser  
225 230 235 240

CAG TTA GGA GAA GAT TAT ATT CAA TTG CAT AAA CTT CTA AGA AAG TCC 830  
Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser  
245 250 255

ACC TTC AAA AAT GCA AAA CTC TAT GGT CCT GAT GTT GGT CAG CCT CGA 878  
Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg  
260 265 270

AGA AAG ACG GCT AAG ATG CTG AAG AGC TTC CTG AAG GCT GGT GGA GAA 926  
Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu  
275 280 285

GTG ATT GAT TCA GTT ACA TGG CAT CAC TAC TAT TTG AAT GGA CGG ACT 974  
Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr  
290 295 300

GCT ACC AGG GAA GAT TTT CTA AAC CCT GAT GTA TTG GAC ATT TTT ATT 1019  
Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile  
305 310 315 320

TCA TCT GTG CAA AAA GTT TTC CAG GTG GTT GAG AGC ACC AGG CCT GGC 1067  
Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly  
325 330 335

AAG AAG GTC TGG TTA GGA GAA ACA AGC TCT GCA TAT GGA GGC GGA GCG 1115  
Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala  
340 345 350

CCC TTG CTA TCC GAC ACC TTT GCA GCT GGC TTT ATG TGG CTG GAT AAA 1163  
Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys  
355 360 365

TTG GGC CTG TCA GCC CGA ATG GGA ATA GAA GTG GTG ATG AGG CAA GTA 1211  
Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val  
370 375 380

TTC TTT GGA GCA GGA AAC TAC CAT TTA GTG GAT GAA AAC TTC GAT CCT 1259  
Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro  
385 390 395 400

TTA CCT GAT TAT TGG CTA TCT CTT CTG TTC AAG AAA TTG GTG GGC ACC 1307  
Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr  
405 410 415

AAG GTG TTA ATG GCA AGC GTG CAA GGT TCA AAG AGA AGG AAG CTT CGA 1355  
Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg

420                      425                      430  
 5      GTA TAC CTT CAT TGC ACA AAC ACT GAC AAT CCA AGG TAT AAA GAA GGA 1403  
       Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly  
              435                      440                      445  
 10     GAT TTA ACT CTG TAT GCC ATA AAC CTC CAT AAC GTC ACC AAG TAC TTG 1451  
       Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu  
              450                      455                      460  
 15     CGG TTA CCC TAT CCT TTT TCT AAC AAG CAA GTG GAT AAA TAC CTT CTA 1499  
       Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu  
              465                      470                      475                      480  
 20     AGA CCT TTG GGA CCT CAT GGA TTA CTT TCC AAA TCT GTC CAA CTC AAT 1547  
       Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn  
                              485                      490                      495  
 25     GGT CTA ACT CTA AAG ATG GTG GAT GAT CAA ACC TTG CCA CCT TTA ATG 1595  
       Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met  
                              500                      505                      510  
 30     GAA AAA CCT CTC CGG CCA GGA AGT TCA CTG GGC TTG CCA GCT TTC TCA 1643  
       Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser  
                              515                      520                      525  
 35     TAT AGT TTT TTT GTG ATA AGA AAT GCC AAA GTT GCT GCT TGC ATC TGA 1691  
       Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile  
                              530                      535                      540                      543  
 40     AAA TAA AAT ATA CTA GTC CTG ACA CTG                      1718

## (2) INFORMATION FOR SEQ ID NO:12:

## 30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 824  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12

40      CTGGCAAGAA GGTCTGGTTG GGAGAGACGA GCTCAGCTTA CGGTGGCGGT GCACCCTTGC 60  
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       TGGGCATAGA AGTCGTGATG AGGCAGGTGT TCTTCGGAGC AGGCAACTAC CACTTAGTGG 180  
       ATGAAAACCT TGAGCCTTTA CCTGATTACT GGCTCTCTCT TCTGTTCAAG AAACCTGGTAG 240  
       GTCCCAGGGT GTTACTGTCA AGAGTGAAAG GCCCAGACAG GAGCAAACTC CGAGTGTATC 300  
       TCCACTGCAC TAACGTCTAT CACCCACGAT ATCAGGAAGG AGATCTAACT CTGTATGTCC 360  
       TGAACCTCCA TAATGTCAAC AAGCACTTGA AGGTACCGCC TCCGTTGTTT AGGAAACCAG 420  
 45      TGGATACGTA CCTTCTGAAG CCTTCGGGGC CGGATGGATT ACTTTCAAA TCTGTCCAAC 480  
       TGAACGGTCA AATTCTGAAG ATGGTGGATG AGCAGACCCT GCCAGCTTTG ACAGAAAAAC 540  
       CTCTCCCCGC AGGAAGTGCA CTAAGCCTGC CTGCCCTTTC CTATGGTTTT TTTGTCAATA 600  
       GAAATGCCAA AATCGCTGCT TGTATATGAA AATAAAAGGC ATACGGTACC CCTGAGACAA 660  
       AAGCCGAGGG GGGTGTATT CATAAAACAA AACCCTAGTT TAGGAGGCCA CCTCCTTGCC 720  
       GAGTTCCAGA GCTTCGGGAG GGTGGGGTAC ACTTCAGTAT TACATTCACT GTGGTGTCT 780  
 50      CTCTAAGAAG AATACTGCAG GTGGTGACAG TTAATAGCAC TGTG                      824

## (2) INFORMATION FOR SEQ ID NO:13:

## 55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1899  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13

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5      GGGAAAGCGA GCAAGGAAGT AGGAGAGAGC CGGGCAGGCG GGGCGGGGTT GGATTGGGAG 60
      CAGTGGGAGG GATGCAGAAG AGGAGTGGGA GGGATGGAGG GCGCAGTGGG AGGGGTGAGG 120
      AGGCGTAACG GGGCGGAGGA AAGGAGAAAA GGGCGCTGGG GCTCGGCGGG AGGAAGTGCT 180
      AGAGCTCTCG ACTCTCCGCT GCGCGGCAGC TGGCGGGGGG AGCAGCCAGG TGAGCCCAAG 240
      ATGCTGCTGC GCTCGAAGCC TGCCTGCCC GCGCCGCTGA TGCTGCTGCT CTTGGGGCCG 300
10     CTGGGTCCCC TCTCCCTGG CGCCCTGCCG CGACCTGCCG AAGCACAGGA CGTCGTGGAC 360
      CTGGACTTCT TCACCCAGGA GCCGCTGCAC CTGGTGAGCC CCTCGTTCTT GTCCGTCACC 420
      ATTGACGCCA ACCTGGCCAC GGACCCGCGG TTCTCATCC TCCTGGGTTC TCCAAAGCTT 480
      CGTACCTTGG CCAGAGGCTT GTCTCCTGCG TACCTGAGGT TTGGTGGCAC CAAGACAGAC 540
      TTCTTAATTT TCGATCCCAA GAAGGAATCA ACCTTTGAAG AGAGAAGTTA CTGGCAATCT 600
      CAAGTCAACC AGGATATTTG CAAATATGGA TCCATCCCTC CTGATGTGGA GGAGAAAGTTA 660
15     CGGTTCGAAT GGCCCTACCA GGAGCAATTG CTACTCCGAG AACACTACCA GAAAAAGTTT 720

      AAGAACAGCA CCTACTCAAG AAGCTCTGTA GATGTGCTAT ACACTTTTGC AAAGTCTCA 780
      GGACTGGACT TGATCTTTGG CCTAAATGCG TTATTAAGAA CAGCAGATTT GCACTGGAAC 840
      AGTTCTAATG CTCAGTTGCT CCTGGACTAC TGCTCTTCCA AGGGGTATAA CATTCTTTGG 900
20     GAAGTAGGCA ATGAACCTAA CAGTTTCCTT AAGAAGGCTG ATATTTTCAT CAATGGGTCG 960
      CAGTTAGGAG AAGATTATAT TCAATTGCAT AAAGTCTTAA GAAAGTCCAC CTTCAAAAT 1020
      GCAAAACTCT ATGGTCTGTA TGTTGGTCAG CCTCGAAGAA AGACGGCTAA GATGCTGAAG 1080
      AGCTTCCTGA AGGCTGGTGG AGAAGTGATT GATTCAGTTA CATGGCATCA CTACTATTG 1140
      AATGGACGGA CTGCTACCAG GGAAGATTTT CTAACCCCTG ATGTATTGGA CATTYYYATT 1200
      TCATCTGTGC AAAAAGTTTT CCAGGTGGTT GAGAGCACCA GGCCTGGCAA GAAGGTCTGG 1260
25     TTAGGAGAAA CAAGCTCTGC ATATGGAGGC GGAGCGCCCT TGCTATCCGA CACCTTTGCA 1320
      GCTGGCTTTA TGTGGCTGGA TAAATTGGGC CTGTCAGCCC GAATGGGAAT AGAAGTGGTG 1380
      ATGAGGCAAG TATTCTTTGG AGCAGGAAAC TACCATTAGG TGGATGAAAA CTTGATCCT 1440
      TTACCTGATT ATYGGCTATC TCTTCTGTT AAGAAATTGG TGGGCACCAA GGTGTTAATG 1500
      GCAAGCGTGC AAGGTTCAAA GAGAAGGAAG CTTGAGTAT ACCTTCATTG CACAAACACT 1560
      GACAATCCAA GGTATAAAGA AGGAGATTTA ACTCTGTATG CCATAAACCT CCATAACGTC 1620
30     ACCAAGTACT TGGCGTTACC CTATCCTTTT TCTAACAAGC AAGTGGATAA ATACCTTCTA 1680
      AGACCTTTGG GACCTCATGG ATTACTTTCC AAATCTGTCC AACTCAATGG TCTAACTCTA 1740
      AAGATGGTGG ATGATCAAAAC CTTGCCACCT TTAATGGAAA AACCTCTCCG GCCAGGAAGT 1800
      TCACTGGGCT TGCCAGCTTT CTCATATAGT TTTTGTGTGA TAAGAAATGC CAAAGTTGCT 1860
      GCTTGCATCT GAAAAATAAA TATACTAGTC CTGACACTG 1899

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592
- (B) TYPE: amino acid
- (C) STRANDEDNESS: singl
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14

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	Met	Glu	Gly	Ala	Val	Gly	Gly	Val	Arg	Arg	Arg	Asn	Gly	Ala	Glu
					5					10					15
	Glu	Arg	Arg	Lys	Gly	Arg	Trp	Gly	Ser	Ala	Gly	Gly	Ser	Ala	Arg
					20					25					30
5	Ala	Leu	Asp	Ser	Pro	Leu	Arg	Gly	Ser	Trp	Arg	Gly	Glu	Gln	Pro
					35					40					45
	Gly	Glu	Pro	Lys	Met	Leu	Leu	Arg	Ser	Lys	Pro	Ala	Leu	Pro	Pro
					50					55					60
	Pro	Leu	Met	Leu	Leu	Leu	Gly	Pro	Leu	Gly	Pro	Leu	Ser	Pro	
					65					70					75
10	Gly	Ala	Leu	Pro	Arg	Pro	Ala	Gln	Ala	Gln	Asp	Val	Val	Asp	Leu
					80					85					90
	Asp	Phe	Phe	Thr	Gln	Glu	Pro	Leu	His	Leu	Val	Ser	Pro	Ser	Phe
					95					100					105
	Leu	Ser	Val	Thr	Ile	Asp	Ala	Asn	Leu	Ala	Thr	Asp	Pro	Arg	Phe
					110					115					120
	Leu	Ile	Leu	Leu	Gly	Ser	Pro	Lys	Leu	Arg	Thr	Leu	Ala	Arg	Gly
15					125					130					135
	Leu	Ser	Pro	Ala	Tyr	Leu	Arg	Phe	Gly	Gly	Thr	Lys	Thr	Asp	Phe
					140					145					150
	Leu	Ile	Phe	Asp	Pro	Lys	Lys	Glu	Ser	Thr	Phe	Glu	Glu	Arg	Ser
					155					160					165
	Tyr	Trp	Gln	Ser	Gln	Val	Asn	Gln	Asp	Ile	Cys	Lys	Tyr	Gly	Ser
					170					175					180
20	Ile	Pro	Pro	Asp	Val	Glu	Glu	Lys	Leu	Arg	Leu	Glu	Trp	Pro	Tyr
					185					190					195
	Gln	Glu	Gln	Leu	Leu	Leu	Arg	Glu	His	Tyr	Gln	Lys	Lys	Phe	Lys
					200					205					210
	Asn	Ser	Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe
					215					220					225
25	Ala	Asn	Cys	Ser	Gly	Leu	Asp	Leu	Ile	Phe	Gly	Leu	Asn	Ala	Leu
					230					235					240
	Leu	Arg	Thr	Ala	Asp	Leu	Gln	Trp	Asn	Ser	Ser	Asn	Ala	Gln	Leu
					245					250					255
	Leu	Leu	Asp	Tyr	Cys	Ser	Ser	Lys	Gly	Tyr	Asn	Ile	Ser	Trp	Glu
					260					265					270
	Leu	Gly	Asn	Glu	Pro	Asn	Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe
30					275					280					285
	Ile	Asn	Gly	Ser	Gln	Leu	Gly	Glu	Asp	Tyr	Ile	Gln	Leu	His	Lys
					290					295					300
	Leu	Leu	Arg	Lys	Ser	Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro
					305					310					315
	Asp	Val	Gly	Gln	Pro	Arg	Arg	Lys	Thr	Ala	Lys	Met	Leu	Lys	Ser
35					320					325					330
	Phe	Leu	Lys	Ala	Gly	Gly	Glu	Val	Ile	Asp	Ser	Val	Thr	Trp	His
					335					340					345

	His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg Glu Asp Phe Leu	
	350	355
	Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys Val	360
	365	370
5	Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val Trp Leu	375
	380	385
	Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser	390
	395	400
	Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu	405
	410	415
10	Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val Phe Phe	420
	425	430
	Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu	435
	440	445
	Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr	450
	455	460
	Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu	465
15	470	475
	Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys	480
	485	490
	Glu Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr	495
	500	505
	Lys Tyr Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp	510
20	515	520
	Lys Tyr Leu Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys	525
	530	535
	Ser Val Gln Leu Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln	540
	545	550
	Thr Leu Pro Pro Leu Met Glu Lys Pro Leu Arg Pro Gly Ser Ser	555
25	560	565
	Leu Gly Leu Pro Ala Phe Ser Tyr Ser Phe Phe Val Ile Arg Asn	570
	575	580
	Ala Lys Val Ala Ala Cys Ile	585
	590	592

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1899

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15



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	Leu Ser Val Thr Ile Asp Ala Asn Leu Ala Thr Asp Pro Arg Phe	
	110 115 120	
5	CTC ATC CTC CTG GGT TCT CCA AAG CTT CGT ACC TTG GCC AGA GGC Leu Ile Leu Leu Gly Ser Pro Lys Leu Arg Thr Leu Ala Arg Gly	498 125 130 135
	TTG TCT CCT GCG TAC CTG AGG TTT GGT GGC ACC AAG ACA GAC TTC Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly Thr Lys Thr Asp Phe	543 140 145 150
10	CTA ATT TTC GAT CCC AAG AAG GAA TCA ACC TTT GAA GAG AGA AGT Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe Glu Glu Arg Ser	588 155 160 165
	TAC TGG CAA TCT CAA GTC AAC CAG GAT ATT TGC AAA TAT GGA TCC Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys Tyr Gly Ser	633 170 175 180
15	ATC CCT CCT GAT GTG GAG GAG AAG TTA CGG TTG GAA TGG CCC TAC Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp Pro Tyr	678 185 190 195
	CAG GAG CAA TTG CTA CTC CGA GAA CAC TAC CAG AAA AAG TTC AAG Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe Lys	723 200 205 210
20	AAC AGC ACC TAC TCA AGA AGC TCT GTA GAT GTG CTA TAC ACT TTT Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe	768 215 220 225
	GCA AAC TGC TCA GGA CTG GAC TTG ATC TTT GGC CTA AAT GCG TTA Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu	813 230 235 240
	TTA AGA ACA GCA GAT TTG CAG TGG AAC AGT TCT AAT GCT CAG TTG Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu	858 245 250 255
30	CTC CTG GAC TAC TGC TCT TCC AAG GGG TAT AAC ATT TCT TGG GAA Leu Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu	903 260 265 270
	CTA GGC AAT GAA CCT AAC AGT TTC CTT AAG AAG GCT GAT ATT TTC Ile Gly Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe	948 275 280 285
35	ATC AAT GGG TCG CAG TTA GGA GAA GAT TAT ATT CAA TTG CAT AAA Ile Asn Gly Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys	993 290 295 300
	CTT CTA AGA AAG TCC ACC TTC AAA AAT GCA AAA CTC TAT GGT CCT Leu Leu Arg Lys Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro	1038 305 310 315
	GAT GTT GGT CAG CCT CGA AGA AAG ACG GCT AAG ATG CTG AAG AGC Asp Val Gly Gln Pro Arg Arg Lys Thr Ala Lys Met Leu Lys Ser	1083 320 325 330
45	TTC CTG AAG GCT GGT GGA GAA GTG ATT GAT TCA GTT ACA TGG CAT Phe Leu Lys Ala Gly Gly Glu Val Ile Asp Ser Val Thr Trp His	1128 335 340 345
	CAC TAC TAT TTG AAT GGA CGG ACT GCT ACC AGG GAA GAT TTT CTA His Tyr Tyr Leu Asn Gly Arg Thr Ala Thr Arg Glu Asp Phe Leu	1173 350 355 360
50	AAC CCT GAT GTA TTG GAC ATT TTT ATT TCA TCT GTG CAA AAA GTT Asn Pro Asp Val Leu Asp Ile Phe Ile Ser Ser Val Gln Lys Val	1218 365 370 375
	TTC CAG GTG GTT GAG AGC ACC AGG CCT GGC AAG AAG GTC TGG TTA Phe Gln Val Val Glu Ser Thr Arg Pro Gly Lys Lys Val Trp Leu	1263 380 385 390
55		

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	GGA GAA ACA AGC TCT GCA TAT GGA GGC GGA GCG CCC TTG CTA TCC	1308
	Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala Pro Leu Leu Ser	400 405
5	GAC ACC TTT GCA GCT GGC TTT ATG TGG CTG GAT AAA TTG GGC CTG	1353
	Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys Leu Gly Leu	410 415 420
10	TCA GCC CGA ATG GGA ATA GAA GTG GTG ATG AGG CAA GTA TTC TTT	1398
	Ser Ala Arg Met Tyr His Ile Glu Val Val Met Arg Gln Val Phe	425 430 435
	GGA GCA GGA AAC TAC CAT TTA GTG GAT GAA AAC TTC GAT CCT TTA	1443
	Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro Leu	440 445 450
15	CCT GAT TAT TGG CTA TCT CTT CTG TTC AAG AAA TTG GTG GGC ACC	1488
	Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr	455 460 465
	AAG GTG TTA ATG GCA AGC GTG CAA GGT TCA AAG AGA AGG AAG CTT	1533
	Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu	470 475 480
20	CGA GTA TAC CTT CAT TGC ACA AAC ACT GAC AAT CCA AGG TAT AAA	1578
	Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys	485 490 495
25	GAA GGA GAT TTA ACT CTG TAT GCC ATA AAC CTC CAT AAC GTC ACC	1623
	Glu Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr	500 505 510
	AAG TAC TTG CGG TTA CCC TAT CCT TTT TCT AAC AAG CAA GTG GAT	1668
	Lys Tyr Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp	515 520 525
30	AAA TAC CTT CTA AGA CCT TTG GGA CCT CAT GGA TTA CTT TCC AAA	1713
	Lys Tyr Leu Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys	530 535 540
	TCT GTC CAA CTC AAT GGT CTA ACT CTA AAG ATG GTG GAT GAT CAA	1758
	Ser Val Gln Leu Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln	545 550 555
35	ACC TTG CCA CCT TTA ATG GAA AAA CCT CTC CGG CCA GGA AGT TCA	1803
	Thr Leu Pro Pro Leu Met Glu Lys Pro Leu Arg Pro Gly Ser Ser	560 565 570
40	CTG GGC TTG CCA GCT TTC TCA TAT AGT TTT TTT GTG ATA AGA AAT	1848
	Leu Gly Leu Pro Ala Phe Ser Tyr Ser Phe Phe Val Ile Arg Asn	575 580 585
	GCC AAA GTT GCT GCT TGC ATC TGA AAA TAA AAT ATA CTA GTC CTG	1893
	Ala Lys Val Ala Ala Cys Ile	590 592
45	ACA CTG	1899

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ATTACTATAG GGCACGCGTG GTCGACGGCC CGGGCTGGTA TTGTCTTAAT GACAAGTTGA 60  
 TAAAGAATTT TGGGTGGTTG ATCTCTTTCC AGCTGCAGTT TAGCGTATGC TGAGGCCAGA 120  
 TTTTTTCAGG CAAAAGTAAA ATACCTGAGA AACTGCCTGG CCAGAGGACA ATCAGATTTT 180  
 GGCTGGCTCA AGTGACAAGC AAGTGTTTAT AAGCTAGATG GGAGAGGAAG GGATGAATAC 240  
 TCCATTGGAG GCTTTACTCG AGGGTCAGAG GGATACCCGG CGCCATCAGA ATGGGATCTG 300  
 GGAGTCGGAA ACCTGGGTT CCCACGAGAG CGCGCAGAAC ACGTGCGTCA GGAAGCCTGG 360  
 TCCGGGATGC CCAGCGCTGC TCCCCGGGCG CTCCTCCCCG GCGGCTCCTC CCCAGGCCTC 420  
 CCGGGCGCTT GGATCCCGGC CATCTCCGCA CCCTTCAAGT GGGTGTGGGT GATTTCTGTA 480  
 GTGAACGTGA CCGCCACCGG GGGGAAAGCG AGCAAGGAAG TAGGAGAGAG CCGGGCAGGC 540  
 GGGGCGGGT TGGATGGGA GCAGTGGGAG GGATGCAGAA GAGGAGTGGG AGGG 594

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

CCCCAGGAGC AGCAGCATCA G 21

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

AGGCTTCGAG CGCAGCAGCA T 21

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

GTAATACGAC TCACTATAGG GC 22

## (2) INFORMATION FOR SEQ 10 NO:20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

ACTATAGGGC ACGCGTGGT 19

(2) INFORMATION FOR SEQ ID NO:21: .

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

CTTGGGCTCA CCTGGGTGCT C 21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22

AGCTCTGTAG ATGTGCTATA CAC 23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

GCATCTTAGC CGTCTTTCTT CG 22

## Claims

1. An isolated polynucleotide fragment comprising a polynucleotide sequence encoding a polypeptide having heparanase catalytic activity, wherein said polypeptide shares at least 70% homology with SEQ ID NOs: 10 or 14 or a functional fragment thereof having heparanase catalytic activity.
2. The polynucleotide fragment of claim 1, wherein said polynucleotide sequence includes nucleotides 63 - 1691 of

SEQ ID NO: 9 or nucleotides 139 - 1869 of SEQ ID NO: 13.

3. The polynucleotide fragment according to claim 1 or 2, wherein said polynucleotide sequence includes nucleotides 63 - 721 of SEQ ID NO- 9.
4. The polynucleotide, fragment of claim 1, wherein said polynucleotide is as set forth in SEQ ID NO: 9 or 13.
5. The polynucleotide fragment of claim 1, wherein said polypeptide includes an amino acid sequence as set forth in SEQ ID NOs: 10 or 14.
6. A polynucleotide fragment comprising a polynucleotide sequence at least 70% homologous with SEQ ID NOs: 9 or 13, said polynucleotide sequence encoding a polypeptide having heparanase catalytic activity.
7. The polynucleotide fragment of any preceding claim, wherein said polynucleotide sequence is selected from the group consisting of double stranded DNA, single stranded DNA and RNA.
8. A vector comprising a polynucleotide fragment according to any preceding claim.
9. A host cell comprising an exogenous polynucleotide fragment according to any of claims 1 to 7.
10. A recombinant protein, which is a polypeptide of 543 amino acids as set forth in SEQ ID NO: 10 with a calculated molecular weight of 61,192 daltons or a functional part thereof
11. A polypeptide of 592 amino acids as set forth in SEQ ID NO: 14 with a calculated molecular weight of 66,407 daltons or a functional part thereof.
12. A pharmaceutical composition comprising, as an active ingredient, the isolated protein/polypeptide according to claim 10 or 11 and a pharmaceutically acceptable carrier.
13. A medical device containing, as an active ingredient, an isolated protein/polypeptide according to claim 10 or 11.
14. A heparanase overexpression system comprising a cell overexpressing heparanase sharing at least 70% homology with SEQ ID Nos: 10 or 14 and encoded by a polynucleotide fragment as claimed in any one of claims 1 to 7.
15. A method of identifying a chromosome region harbouring a heparanase gene in a chromosome spread comprising the steps of:
  - (a) hybridizing the chromosome spread with a tagged polynucleotide probe according to claims 6 or 7,
  - (b) washing the chromosome spread, thereby removing excess of non-hybridized probe; and
  - (c) searching for signals associated with said hybridized tagged probe, wherein detected signals being indicative of a chromosome region harbouring a heparanase gene.

#### Patentansprüche

1. Isoliertes Polynucleotidfragment, umfassend eine Polynucleotidsequenz, die ein Polypeptid codiert, das Heparanase-katalytische Aktivität besitzt, wobei das Polypeptid mindestens 70% Homologie mit SEQ ID NR:10 oder 14 oder einem funktionalen Fragment davon mit Heparanase-katalytischer Aktivität aufweist.
2. Polynucleotidfragment nach Anspruch 1, wobei die Polynucleotidsequenz Nucleotide 63-1691 von SEQ ID NR:9 oder Nucleotide 139-1869 von SEQ ID NR:13 umfasst.
3. Polynucleotidfragment nach Anspruch 1 oder 2, wobei die Polynucleotidsequenz Nucleotide 63-721 von SEQ ID NR:9 umfasst.
4. Polynucleotidfragment nach Anspruch 1, wobei das Polynucleotid wie in SEQ ID NR:9 oder 13 dargestellt ist.
5. Polynucleotidfragment nach Anspruch 1, wobei das Polypeptid eine wie in SEQ ID NR:10 oder 14 dargestellte

Aminosäuresequenz umfasst.

6. Polynucleotidfragment, umfassend eine Polynucleotidsequenz mit mindestens 70% Homologie mit SEQ ID NR:9 oder 13, wobei die Polynucleotidsequenz ein Polypeptid mit Heparanase-katalytischer Aktivität codiert.
7. Polynucleotidfragment nach einem der vorangegangenen Ansprüche, wobei die Polynucleotidsequenz ausgewählt ist aus einer Gruppe bestehend aus doppelsträngiger DNA, einzelsträngiger DNA und RNA.
8. Vektor, umfassend ein Polynucleotidfragment nach einem der vorangegangenen Ansprüche.
9. Wirtszelle, umfassend ein exogenes Polynucleotidfragment nach einem der Ansprüche 1 bis 7.
10. Rekombinantes Protein, welches ein Polypeptid mit 543 Aminosäuren ist, wie dargestellt in SEQ ID NR:10, mit einem berechneten Molekulargewicht von 61.192 Dalton, oder ein funktionelles Fragment davon.
11. Polypeptid mit 592 Aminosäuren, wie dargestellt in SEQ ID NR:14, mit einem berechneten Molekulargewicht von 66.407 Dalton, oder ein funktionelles Fragment davon.
12. Arzneimittel, umfassend, als einen aktiven Bestandteil, das isolierte Protein/Polypeptid nach Anspruch 10 oder 11 und einen pharmazeutisch verträglichen Träger.
13. Medizinprodukt, enthaltend, als einen aktiven Bestandteil, ein isoliertes Protein/Polypeptid nach Anspruch 10 oder 11.
14. Heparanase-Überexpressionssystem, umfassend eine Zelle, welche eine Heparanase überexprimiert, die mindestens 70% Homologie mit SEQ ID NR:10 oder 14 aufweist und durch ein Polynucleotidfragment gemäß einem der Ansprüche 1 bis 7 codiert wird.
15. Verfahren zur Identifizierung einer Chromosomenregion, die ein Heparanasegen enthält, in einer Chromosomenansammlung, umfassend die Schritte:

- (a) Hybridisieren der Chromosomenansammlung mit einer markierten Polynucleotidsonde nach einem der Ansprüche 6 oder 7;
- (b) Waschen der Chromosomenansammlung, wobei ein Überschuss von nicht hybridisierter Sonde entfernt wird; und
- (c) Suchen nach Signalen, die mit der hybridisierten markierten Sonde assoziiert sind, wobei der Nachweis von Signalen auf eine Chromosomenregion hinweist, die ein Heparanasegen enthält.

## Revendications

1. Fragment polynucléotidique isolé comprenant une séquence polynucléotidique codant un polypeptide ayant une activité catalytique héparanase, dans lequel ledit polypeptide possède au moins 70% d'homologie avec SEQ ID NO : 10 ou 14 ou un fragment fonctionnel de celles-ci ayant une activité catalytique héparanase.
2. Fragment polynucléotidique selon la revendication 1, dans lequel la séquence polynucléotidique inclut les nucléotides 63 - 1691 de SEQ ID NO : 9 ou les nucléotides 139 -1869 de SEQ ID NO 13.
3. Fragment polynucléotidique selon la revendication 1 ou 2, dans lequel la séquence polynucléotidique inclut les nucléotides 63 - 721 de SEQ ID NO : 9.
4. Fragment polynucléotidique selon la revendication 1, dans lequel ledit polynucléotide est tel que représenté dans SEQ ID NO : 9 ou 13.
5. Fragment polynucléotidique selon la revendication 1, dans lequel ledit polypeptide inclut une séquence d'acides aminés telle que représentée dans SEQ ID NO : 10 ou 14.
6. Fragment polynucléotidique comprenant une séquence polynucléotidique au moins 70% homologue à SEQ ID

NOs : 9 ou 13, ladite séquence polynucléotidique codant un polypeptide ayant une activité catalytique héparanase.

7. Fragment polynucléotidique selon l'une quelconque des revendications précédentes, dans lequel ladite séquence polynucléotidique est choisie dans le groupe constitué d'ADN double-brin, d'ADN simple-brin et d'ARN.
8. Vecteur comprenant un fragment polynucléotidique selon l'une quelconque des revendications précédentes.
9. Cellule hôte comprenant un fragment polynucléotidique exogène selon l'une des revendications 1 à 7.
10. Protéine recombinante, qui est un polypeptide de 543 acides aminés tel que représenté dans SEQ ID NO : 10 ayant un poids moléculaire calculé de 61 192 daltons, ou une partie fonctionnelle de celui-ci.
11. Polypeptide de 592 acides aminés tel que représenté dans SEQ ID NO : 14 ayant un poids moléculaire calculé de 66 407 daltons, ou une partie fonctionnelle de celui-ci.
12. Composition pharmaceutique comprenant, en tant qu'ingrédient actif, la(le) protéine/polypeptide isolé(e) selon la revendication 10 ou 11 et un support acceptable sur le plan pharmaceutique.
13. Dispositif médical contenant, en tant qu'ingrédient actif, un(e) protéine/polypeptide isolé(e) selon la revendication 10 ou 11.
14. Système pour la sur-expression d'une héparanase, comprenant une cellule sur-exprimant une héparanase ayant au moins 70% d'homologie avec SEQ ID NO : 10 ou 14 et codée par un fragment polynucléotidique tel que revendiqué dans l'une des revendications 1 à 7.
15. Méthode pour identifier une région chromosomique portant un gène héparanase à partir d'un étalement de chromosomes, comprenant les étapes consistant à :

- (a) hybrider l'étalement de chromosomes avec une sonde polynucléotidique étiquetée selon les revendications 6 ou 7,
- (b) laver l'étalement de chromosomes, éliminant ainsi l'excès de sonde non-hybridée ; et
- (c) rechercher des signaux associés à ladite sonde étiquetée, les signaux détectés étant indicatifs d'une région chromosomique portant un gène héparanase.



1 CTAGAGCTTTTCAGACTCTCCGCTGCGCGGAGCTGGCGGGGGAGCAGCCAGGTGAGCCCA

61 AGATGCTGCTGCGCTCGAAGCCTGCGCTGCCGCGCCGCTGATGCTGCTGCTCTCTGGGGC  
M L L R S K P A L P P P L M L L L L G P

121 CGCTGGGCTCCCTCTCCCTGCGCGCTGCCCGGACCTGCECAAGCACAGGACGCTCTGG  
L G P L S P G A L P R P A Q A Q D V V D

181 ACCTGGACTTCTCTACCCAGGAGCGCTGCACTGGTGAGCCCCCTCGTTCTCTGTCGGTCA  
L D F F T Q E P L H L V S P S F L S V T

241 CCATTGACCCCAAGCTGGCCACGGACCGCGGTTCTCTCATCTCTCTGGSTTCTCCAAAGC  
I D A N L A T D P R F L I L L G S P K L

301 TTCGTAAGCTTGGCCAGAGGCTTGTCTCTCTGCGTACCTGAGGTTTGGTGGCACCAGACAG  
R T L A R G L S P A Y L R F G G T K T D

361 ACTTCTCTAATTTCGATCCCAAGAGGAATCAACCTTTGAGAGAGAGATTACTGGCAT  
F L I F D P K K E S T F E E R S Y W Q S

421 CTCAGGTCACAGGATATTTCGAATATGGATCCATCCCTCTGATGTGGAGGAGAAST  
Q V N Q D I C K Y G S I P P D V E E K L

481 TACGGTTGGAGTGGCCCTACCGAGGCAATTGCTACTCCGAGAACACTACCAGAAAAST  
R L E W P Y Q E Q L L L R E H Y Q K K F

541 TCAGAGACAGCCCTACTCAAGAAGCTCTGTAGATGTGCTATACACTTTTGCACACTGCT  
K N S T Y S R S S V D V L Y T F A N C S

601 CAGGACTGGACTTATCTTTGGGCTAAATGCGTTATTAAGAACAGCAGATTTCAGTGA  
G I D L I F G L N A L L R T A D L Q W N

661 ACAGTCTCTAATGCTCAAGTGTCTCTGGACTACTGCTCTTCCAGGGGTATACAGATTCTT  
S S N A Q L L L D Y C S S K G Y N I S W

721 GGGACCTAGGCTATGACCTAACAGSTTTCCTTAAGAGGGCTGATATTTCTATCACTAGST  
E L G N E P N S F L K K A D I E I N G S  
(T)

781 CGCAGTTAGGAGAGATTATATTCAATTGCATAAATCTTAAGAGAGTCCACCTTCAAA  
Q L G E D Y I Q L H K L R K S T F K N  
(F)

841 ATGCAAGCTCTATGCTCTGATTTGGTGACGCTCGAAGAGAGAGGCTTAAAGAGCTGA  
A K L Y G P D V G Q P R R K T A K M L K

901 AGAGCTTCTCTAAGGCTGGTGGAGAGTGAATTGATTCAGTTACATGSCATCACTACTAT  
S F L K A G G E V I D S V T W H S Y Y L

961 TGAATGACGCTCTCTACCAGGGAAGATTTTCTAAACCTGATGATGAGAGCTTTT  
N G R T A T R E D F L N P D V L D I F I

1021 TTTCATCTGTGCAAAAAGTTTTCAGGTGGTTGAGAGCACCAGGCTTGGCAGAGAGTCT  
S S V Q K V F Q V V E S T R P G K K V W

1081 GGTAAAGAGAACAGCTCTGCATATGGAGCGGAGCGCCCTTGTATCCGACACCTTGG  
L G E T S S A Y G G G A P L L S D T F A

1141 CAGCTGCTCTATGCTGGCTGGATAAATTGGGCTGTGACGCCGAATGGGATAGAASTGG  
A G F M W L D K L G L S A R M G I E V V

1201 TGATTAAGCAAGTATCTTTGGAGCAGGAACTACCATTAGTGGATGAAPACTTGCAT  
M R Q V T F F G A G N Y H L V D E N F D P

1261 CTTTACTGATTTTGGCTATCTCTCTGTTCAAGAAATTGGTGGGCGCCAGAGGTGTAA  
L P D Y W L S L L F K K L V G T K V L M

1321 TGGCAGGCTGCAAGGTTCAAGAGAGGAAGCTTCGAGTATACCTTCATTGCACAAACA  
A S V Q G S K R R K L R V Y L H C T N T

1381 CTGACATCCAGGTATAAAGAAGGAGATTAACTCTGTATGCCATAAAGCTCCATAGC  
D N P R Y K E G D L T L Y A I N L E N V

1441 TCCCAAGTACTTGGGTTACCTATCTTTTTCTAACAGCAAGTGGATAAATACCTTC  
T K Y L R L P Y P F S N K Q V D K Y L L

1501 TAGAGCTTTGGGACCTCATGGATTACTTTCCAAATCTGTCCAACTCAATGGTCAACTC  
R P L G P B G L L S K S V Q L N G L T L

1561 TAAAGATGGTGGATGATCAACCTTGGCACCTTAATGGAAAAACCTCTCCGGCCAGGAA  
K M V D D Q T L P P L M E K P L R P G S

1621 GTTCTGAGGCTTGGCACTTTCTCATATAGTTTTTTTGTGATAGAAATGCCAAAGTTG  
S L G L P A F S Y S F F V I R N A K V A

FIG. 2

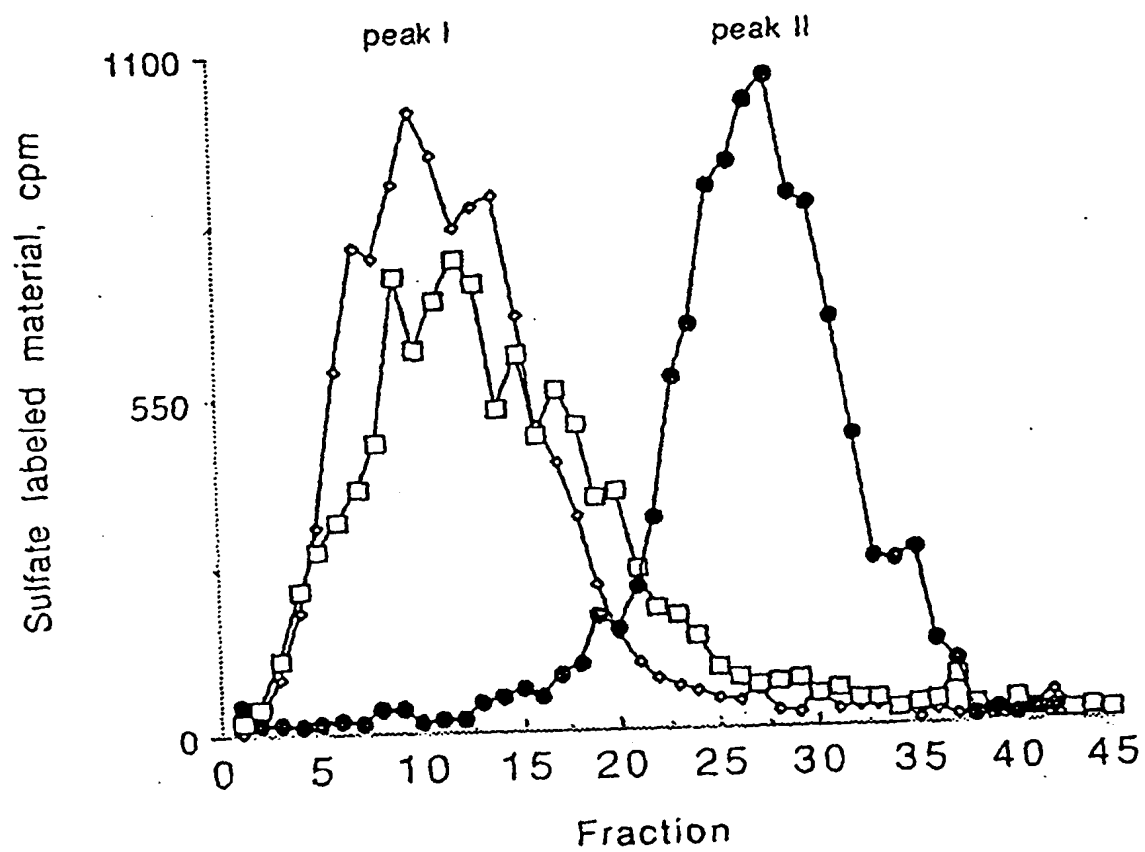


FIG. 3A

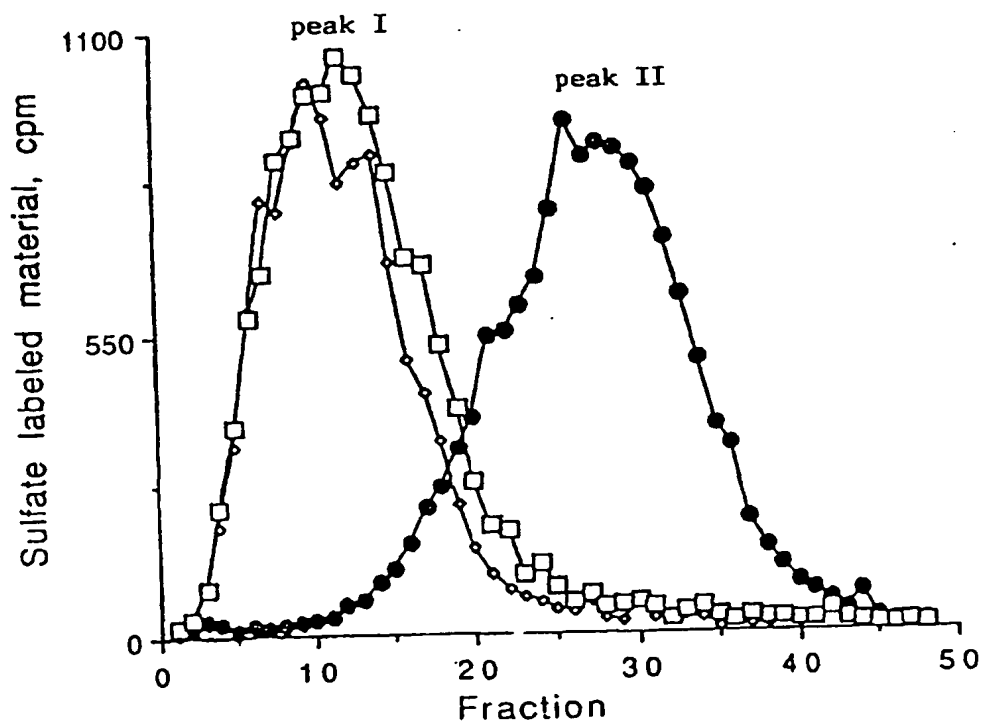


FIG. 3B

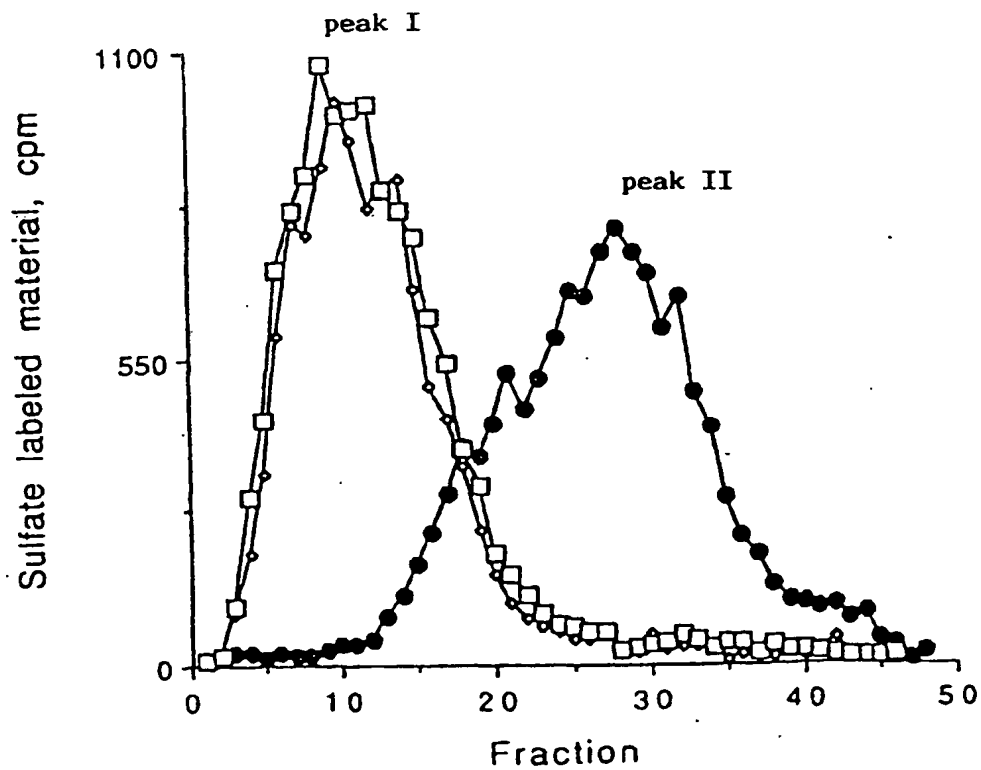


FIG. 4

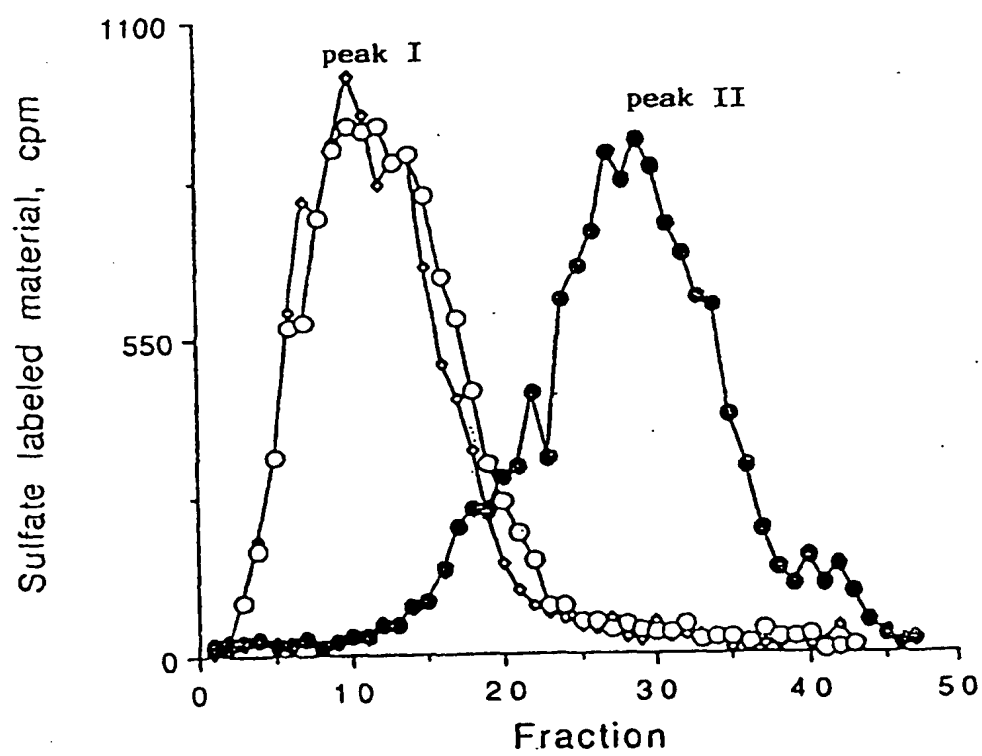


FIG. 5A

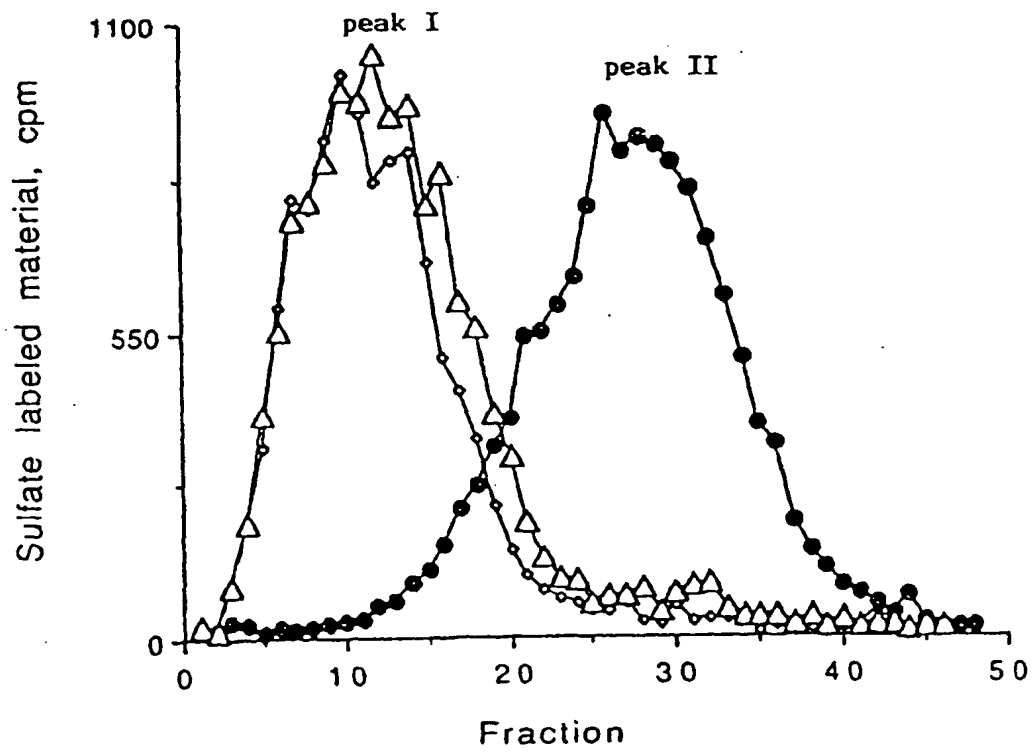


FIG. 5B

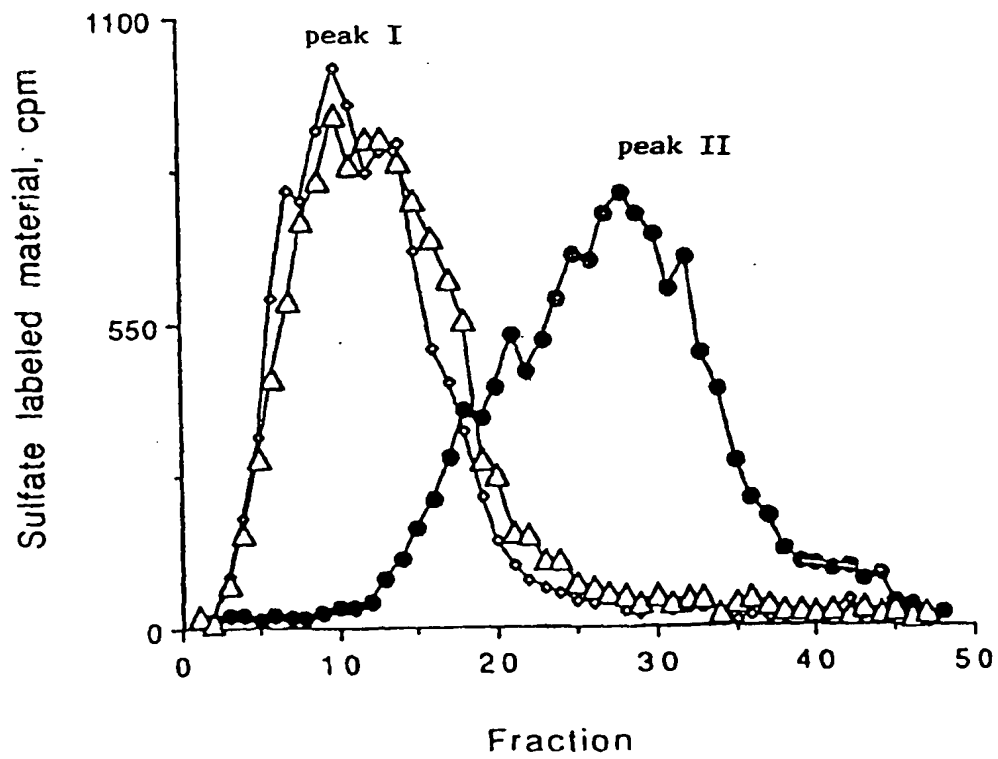


FIG. 6A

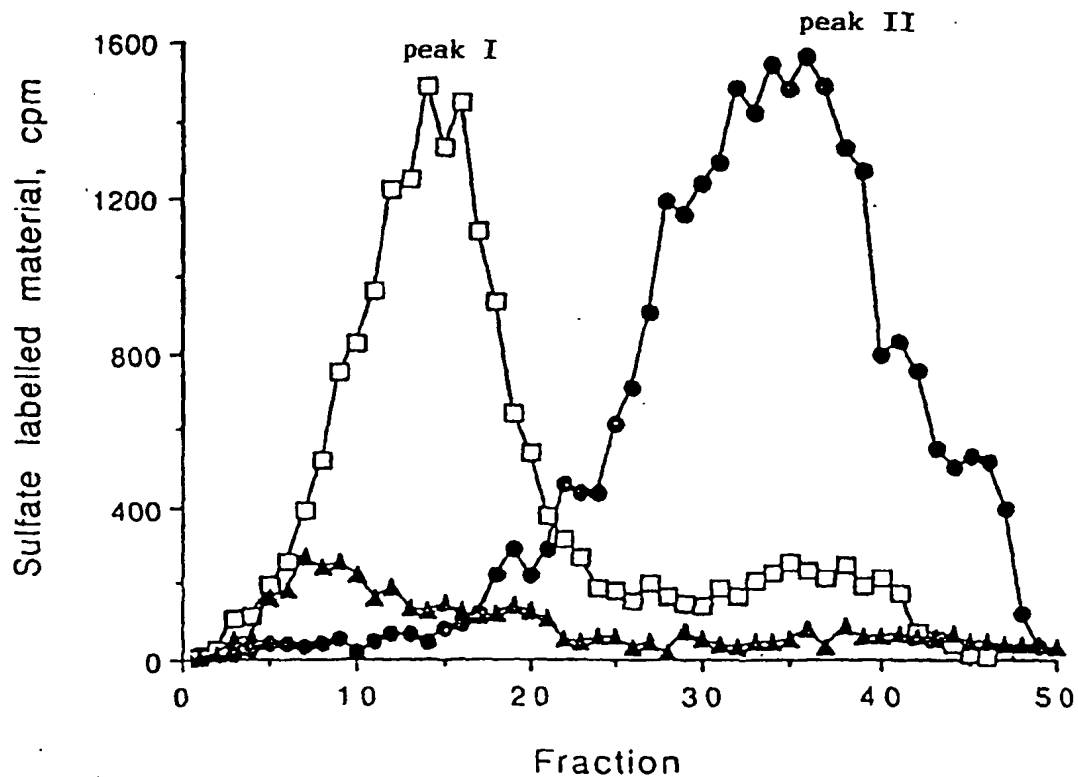


FIG. 6B

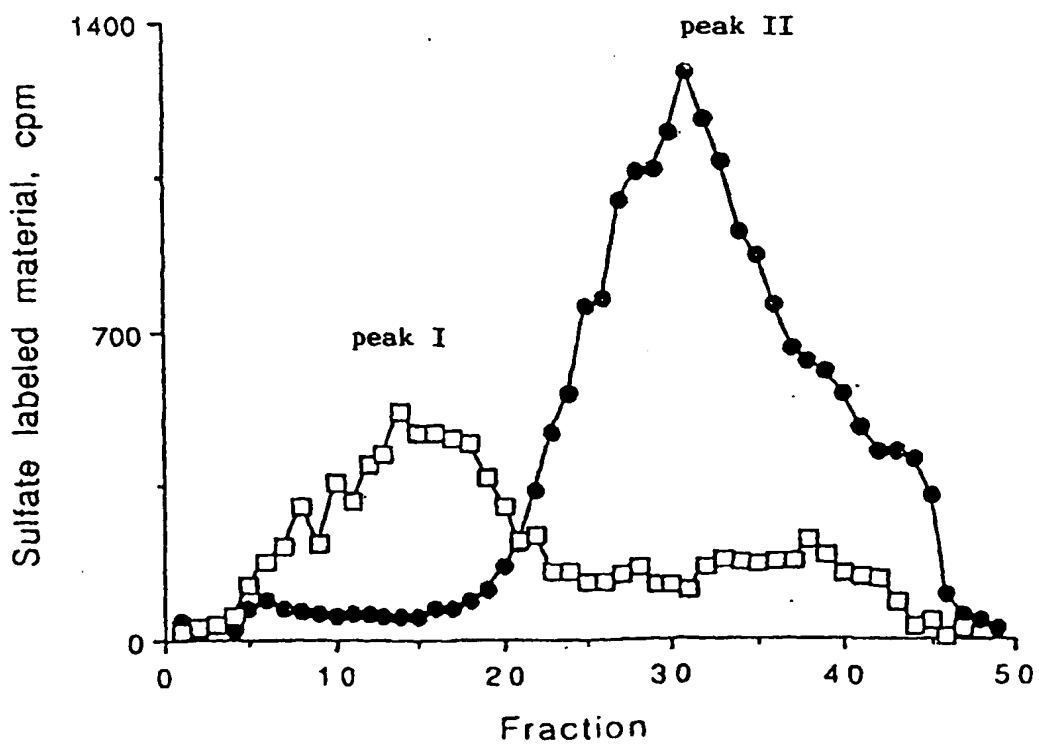


FIG. 7A

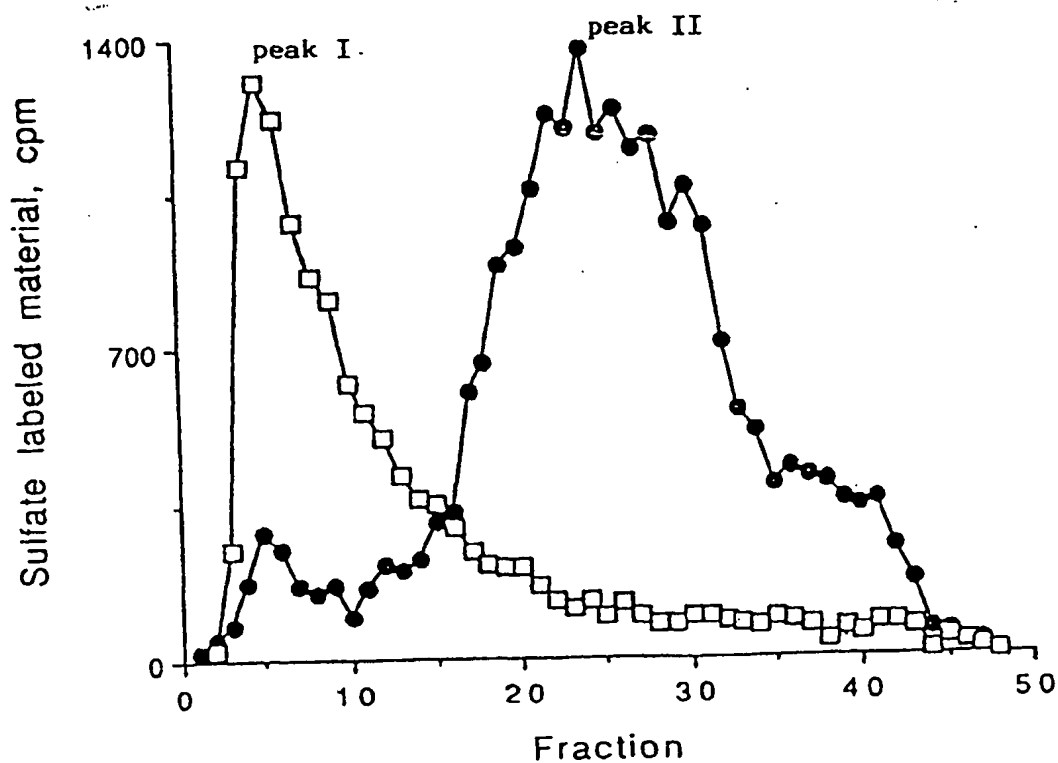


FIG. 7B

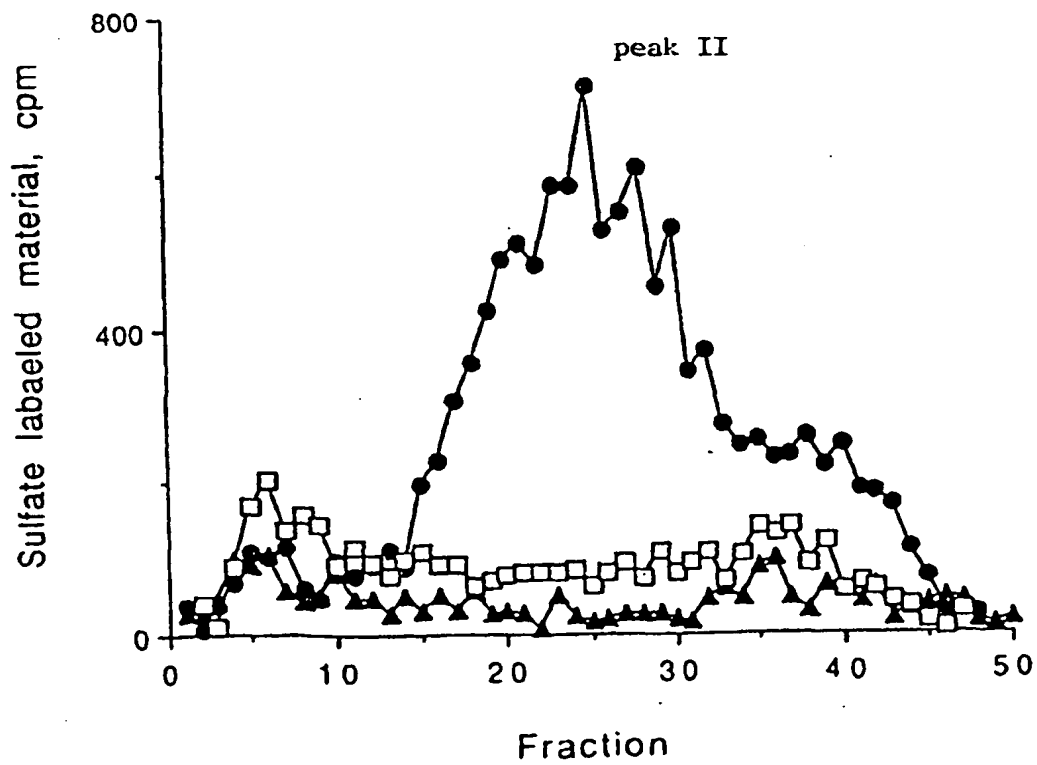


FIG. 8A

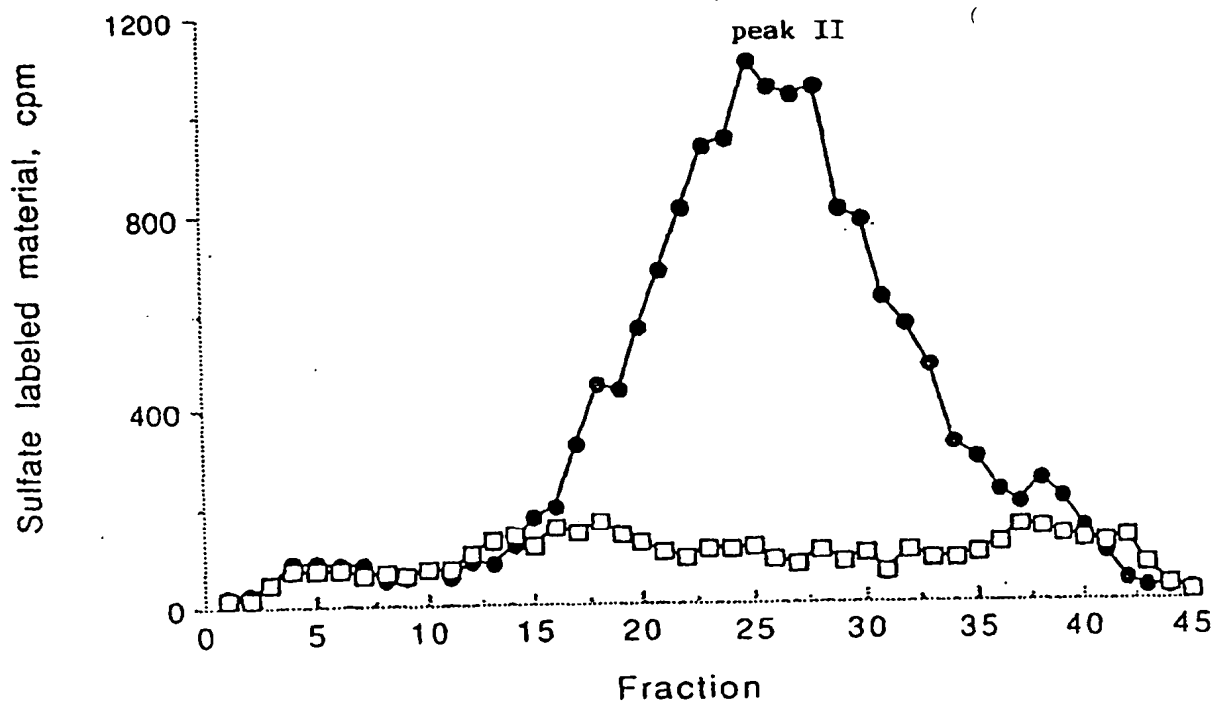


FIG. 8B

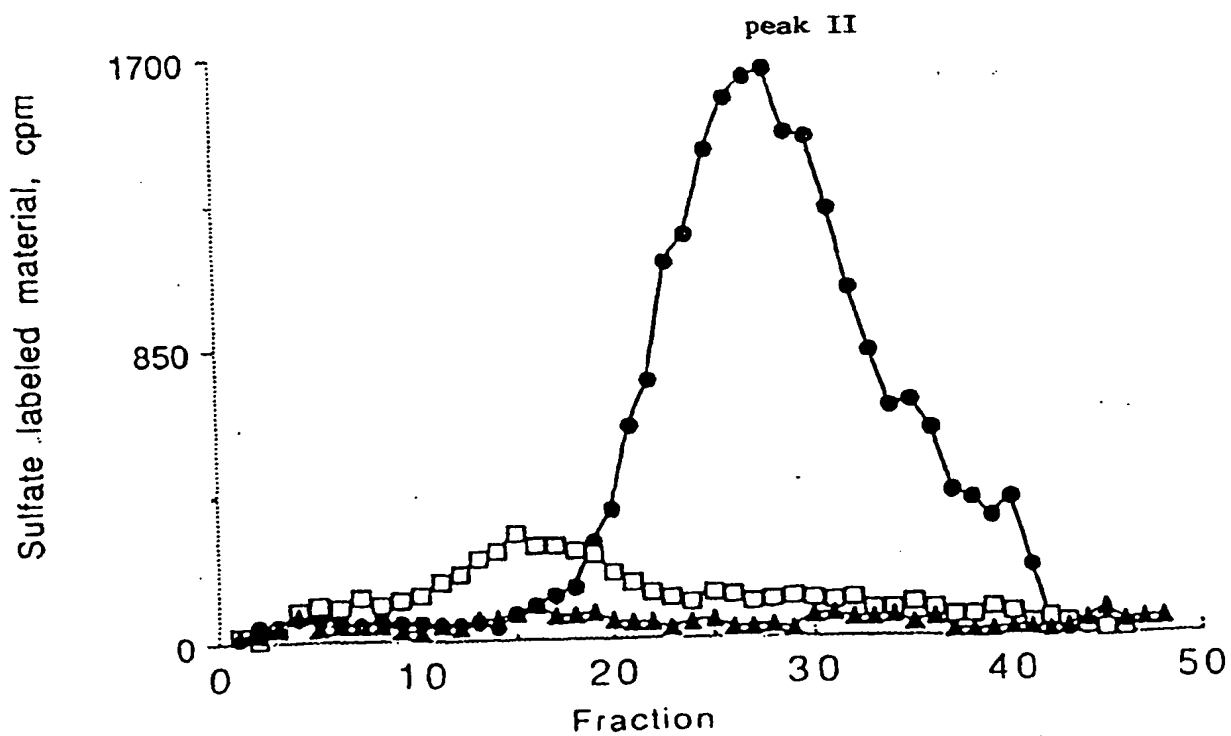




FIG. 9A

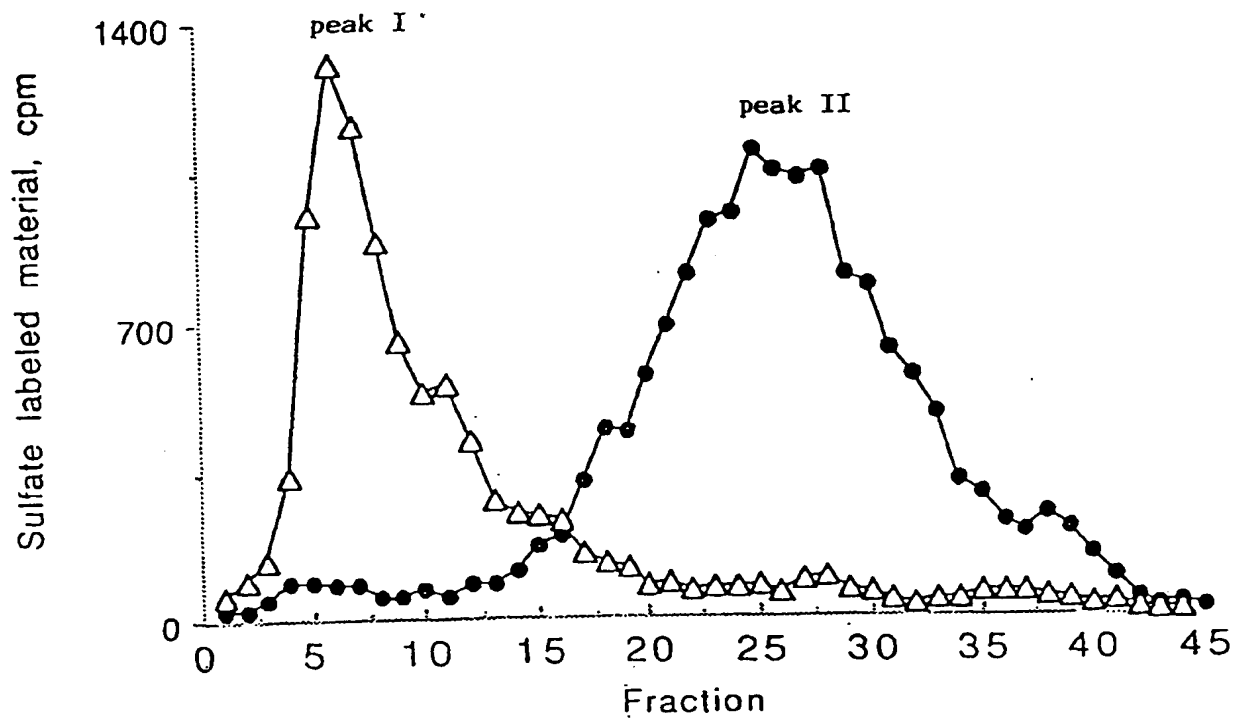
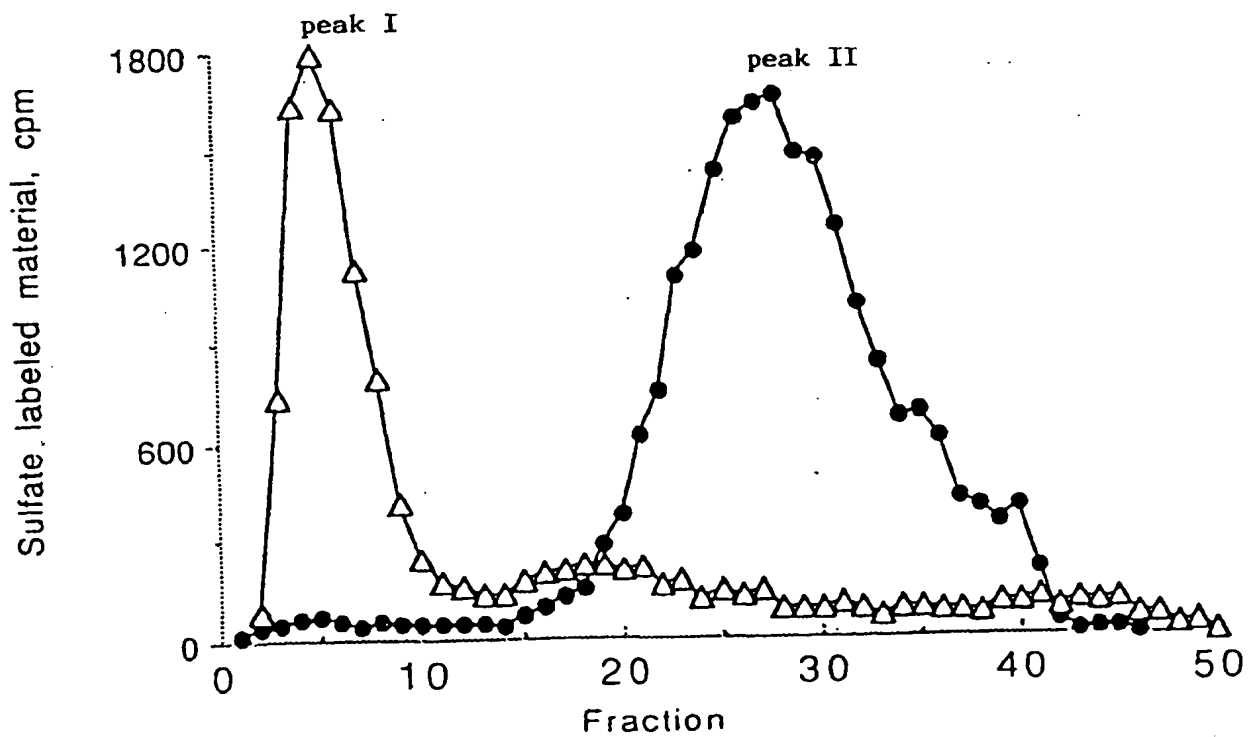


FIG. 9B



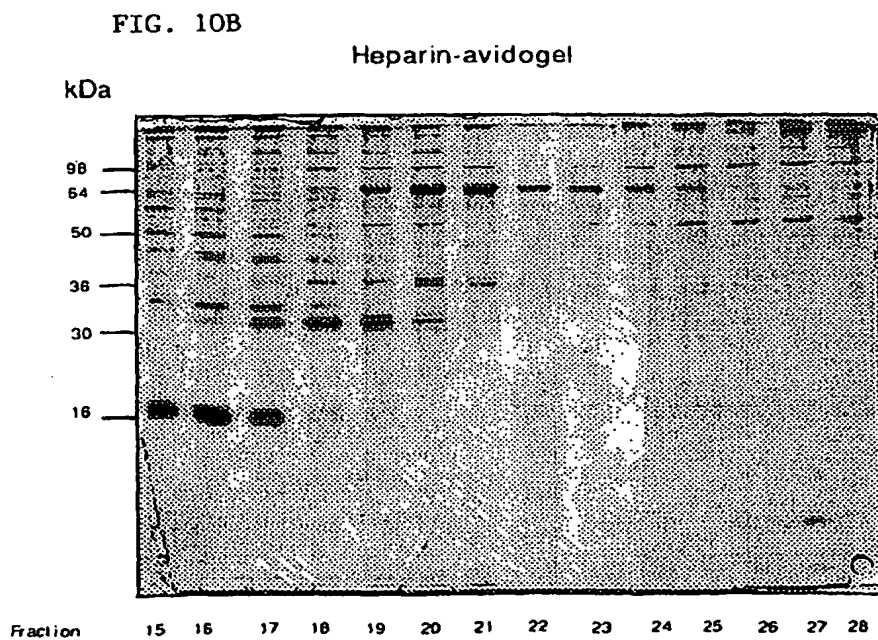
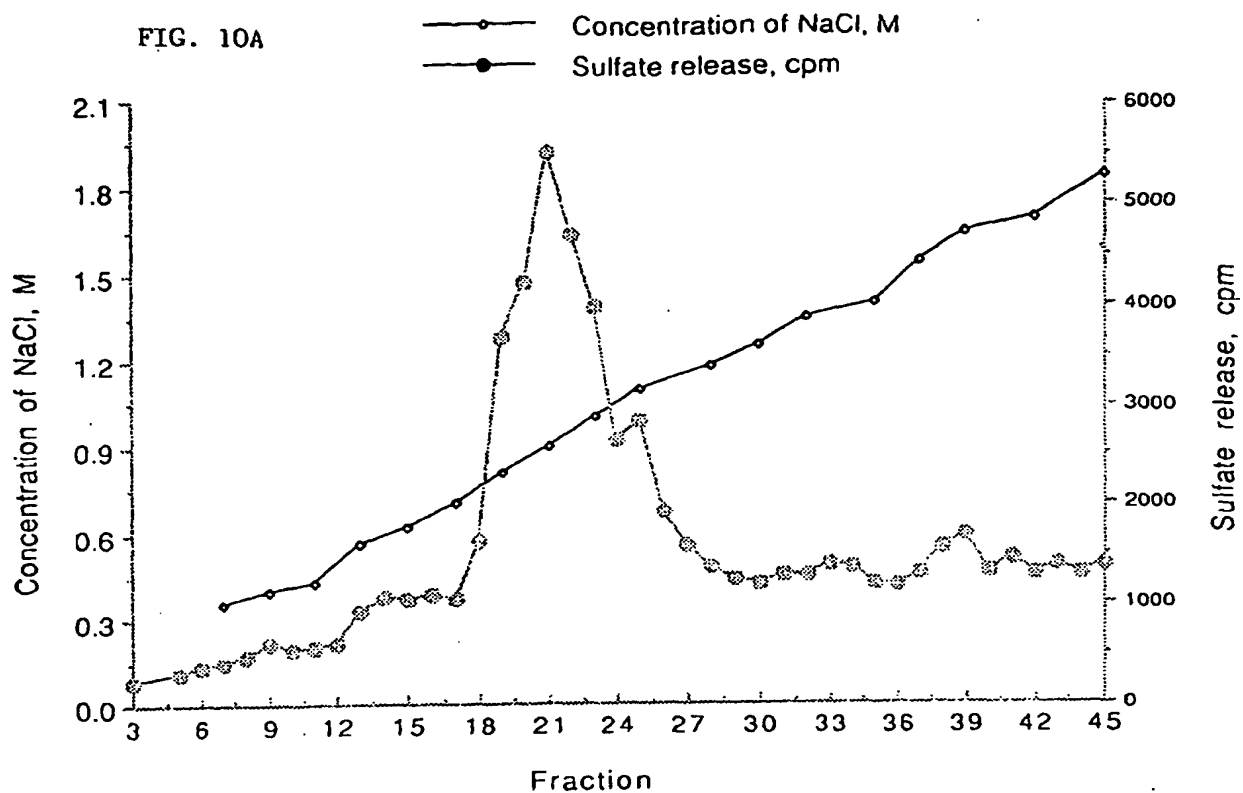


FIG. 11A

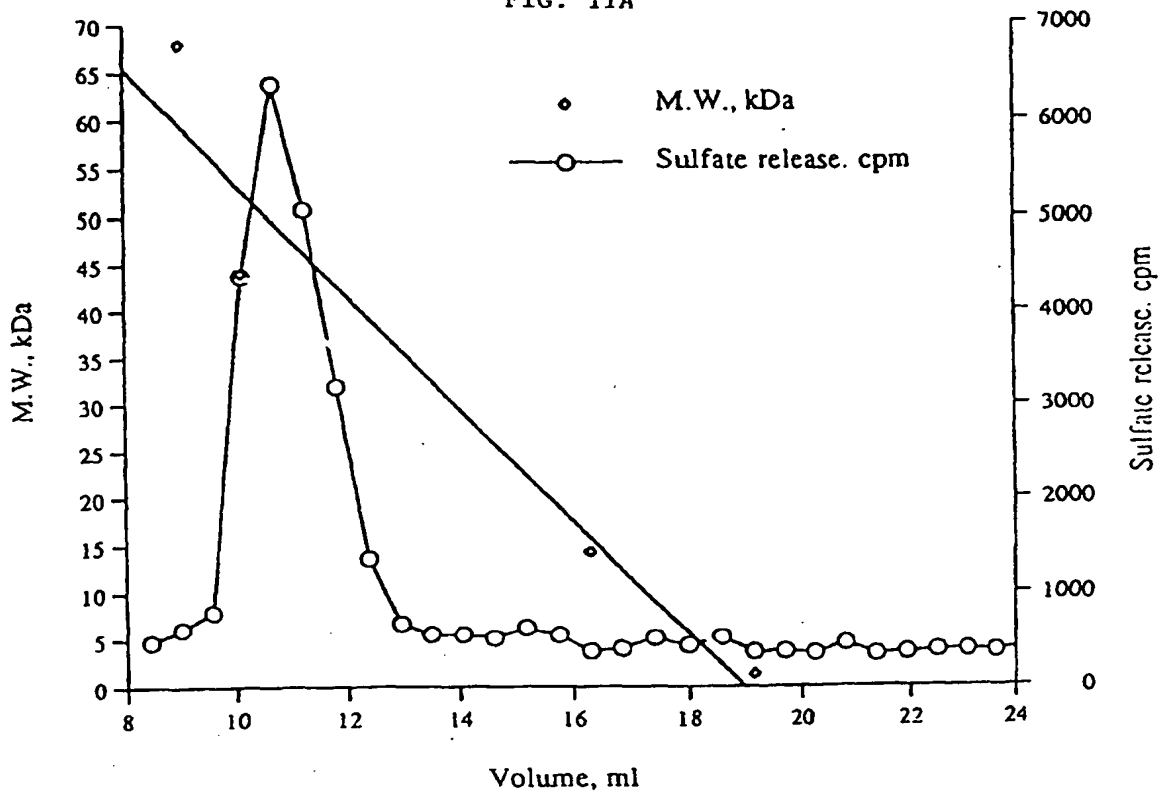


FIG. 11B

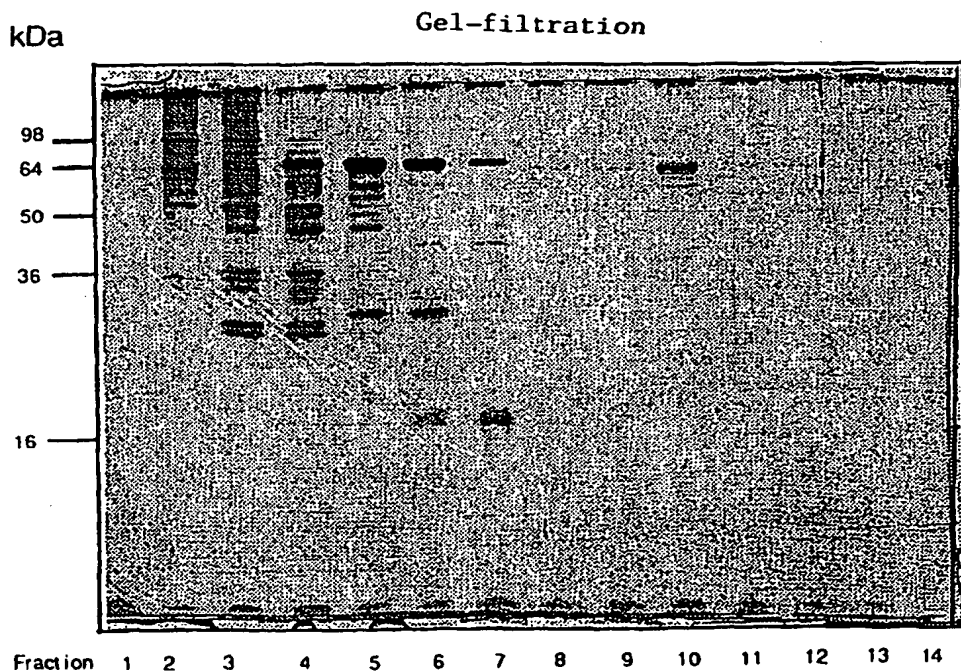


FIG. 12A

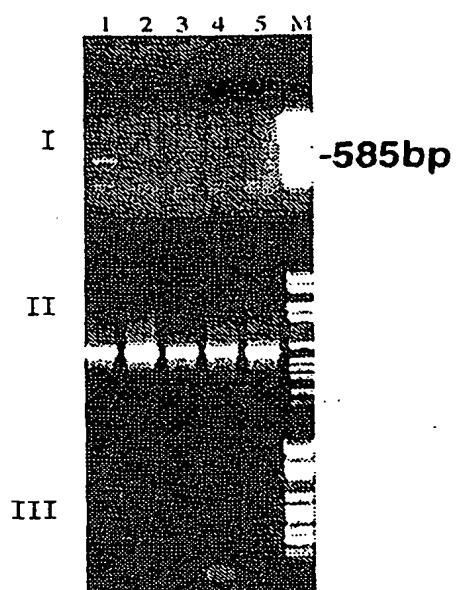


FIG. 12B

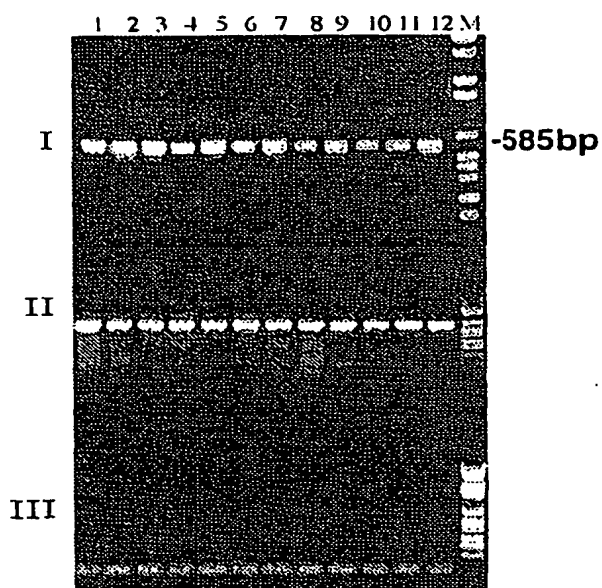


FIG. 12C

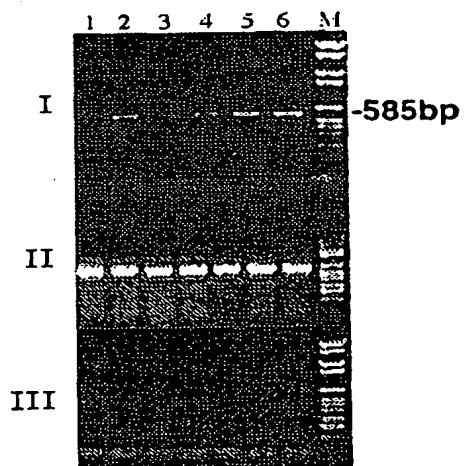


FIG. 12D

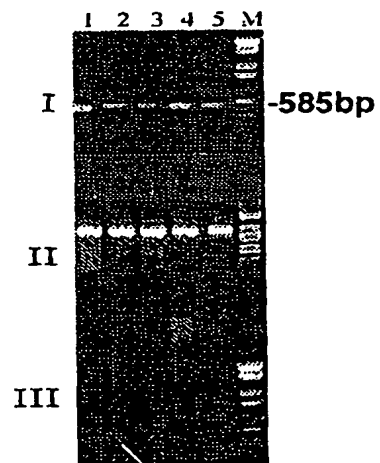


FIG. 12E

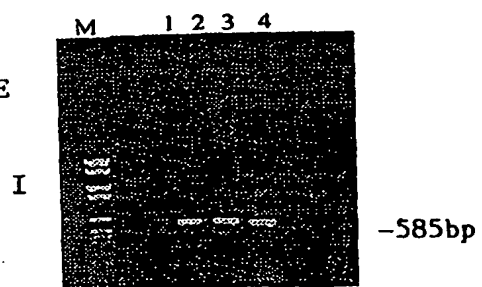


Fig 13

mouse	CTGGCAAGAAGGTCTGGTTGGGAGAGACGAGCTCAGCTTACGGTGGCGGT	50
human	CTGGCAAGAAGGTCTGGTTAGGAGAAACAAGCTCTGCATATGGAGGCGEA	1115
mouse	GCACCCTTGCTGTCCAACACCTTTGCAGCTGGCTTTATGTGGCTGGATAA	100
human	GCGCCCTTGCTATCCGACACCTTTGCAGCTGGCTTTATGTGGCTGGATAA	1165
mouse	ATTGGGCCTGTGACGCCAGATGGGCATAGAAGTCGTGATGAGGCAGGTGT	150
human	ATTGGGCCTGTGACGCCGAATGGGAATAGAAGTGGTGTGAGGCAAGTAT	1215
mouse	TCTTCGGAGCAGGCAACTACCACTTAGTGGATGAAAACCTTTGAGCCTTTA	200
human	TCTTTGGAGCAGGAAACTACCATTTAGTGGATGAAAACCTTCGATCCTTTA	1265
mouse	CCTGATTACTGGCTCTCTCTTCTGTTCAAGAACTGGTAGGTCCCAGGGT	250
human	CCTGATTATTGGCTATCTCTTCTGTTCAAGAAATTGGTGGGCACCAAGGT	1315
mouse	GTTACTGTCAAGAGTGAAAGGCCAGACAGGAGCAAACCTCCGAGTGTATC	300
human	GTTAATGGCAAGCGTGCAAGGTTCAAAGAGAAGGAAGCTTCGAGTATACC	1365
mouse	TCCACTGCACTAACGTCTATCACCACGATATCAGGAAGGAGATCTAACT	350
human	TTCATTGCACAAACACTGACAATCCAAGGTATAAAGAAGGAGATTAACT	1415
mouse	CTGTATGTCCTGAACCTCCATAATGTCACCAAGCACTTGAAGGTACCGCC	400
human	CTGTATGCCATAAACCTCCATAACGTCACCAAGTACTTGCGGTTACCCTA	1465
mouse	TCCGTTGTTTCAGGAAACCAGTGGATACGTACCTTCTGAAGCCTTCGGGGC	450
human	TCCTTTTCTAACAAGCAAGTGGATAAATACCTTCTAAGACCTTTGGGAC	1515
mouse	CGGATGGATTACTTTCCAAATCTGTCCAACCTGAACGGTCAAATTCTGAAG	500
human	CTCATGGATTACTTTCCAAATCTGTCCAACCTCAATGGTCTAACTCTAAAG	1565
mouse	ATGGTGGATGAGCAGACCCTGCCAGCTTTGACAGAAAAACCTCTCCCCGC	550
human	ATGGTGGATGATCAAACCTTGCCACCTTTAATGGAAAAACCTCTCCGGCC	1615
mouse	AGGAAGTGCACTAAGCCTGCCTGCCTTTTCTATGGTTTTTTTGTGATAA	600
human	AGGAAGTTCAGTGGGCTTGCCAGCTTCTCATATAGTTTTTTTGTGATAA	1665
mouse	GAAATGCCAAAATCGCTGCTTGTATATGAAAATAAAA	637
human	GAAATGCCAAGTTGCTGCTTGCATCTGAAAATAAAA	1702

FIG. 14

